

Connecting via Winsock to STN

Welcome to STN International! Enter x:x

LOGINID:ssspt189dxw

PASSWORD:

TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * Welcome to STN International * * * * *

NEWS	1		Web Page for STN Seminar Schedule - N. America
NEWS	2	APR 04	STN AnaVist, Version 1, to be discontinued
NEWS	3	APR 15	WPIDS, WPINDEX, and WPIX enhanced with new predefined hit display formats
NEWS	4	APR 28	EMBASE Controlled Term thesaurus enhanced
NEWS	5	APR 28	IMSRESEARCH reloaded with enhancements
NEWS	6	MAY 30	INPAFAMDB now available on STN for patent family searching
NEWS	7	MAY 30	DGENE, PCTGEN, and USGENE enhanced with new homology sequence search option
NEWS	8	JUN 06	EPFULL enhanced with 260,000 English abstracts
NEWS	9	JUN 06	KOREAPAT updated with 41,000 documents
NEWS	10	JUN 13	USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications
NEWS	11	JUN 19	CAS REGISTRY includes selected substances from web-based collections
NEWS	12	JUN 25	CA/CAPplus and USPAT databases updated with IPC reclassification data
NEWS	13	JUN 30	AEROSPACE enhanced with more than 1 million U.S. patent records
NEWS	14	JUN 30	EMBASE, EMBAL, and LEMBASE updated with additional options to display authors and affiliated organizations
NEWS	15	JUN 30	STN on the Web enhanced with new STN AnaVist Assistant and BLAST plug-in
NEWS	16	JUN 30	STN AnaVist enhanced with database content from EPFULL
NEWS	17	JUL 28	CA/CAPplus patent coverage enhanced
NEWS	18	JUL 28	EPFULL enhanced with additional legal status information from the epline Register
NEWS	19	JUL 28	IFICDB, IFIPAT, and IFIUIDB reloaded with enhancements
NEWS	20	JUL 28	STN Viewer performance improved
NEWS	21	AUG 01	INPADOCDB and INPAFAMDB coverage enhanced
NEWS	22	AUG 13	CA/CAPplus enhanced with printed Chemical Abstracts page images from 1967-1998
NEWS	23	AUG 15	CAOLD to be discontinued on December 31, 2008
NEWS	24	AUG 15	CAPplus currency for Korean patents enhanced
NEWS	25	AUG 25	CA/CAPplus, CASREACT, and IFI and USPAT databases enhanced for more flexible patent number searching
NEWS	26	AUG 27	CAS definition of basic patents expanded to ensure comprehensive access to substance and sequence information
NEWS	27	SEP 18	Support for STN Express, Versions 6.01 and earlier, to be discontinued
NEWS	28	SEP 25	CA/CAPplus current-awareness alert options enhanced to accommodate supplemental CAS indexing of exemplified prophetic substances

NEWS 29 SEP 26 WPIDS, WPINDEX, and WPIX coverage of Chinese and
and Korean patents enhanced
NEWS 30 SEP 29 IFICLS enhanced with new super search field
NEWS 31 SEP 29 EMBASE and EMBAL enhanced with new search and
display fields
NEWS 32 SEP 30 CAS patent coverage enhanced to include exemplified
prophetic substances identified in new Japanese-
language patents

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3,
AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

NEWS HOURS STN Operating Hours Plus Help Desk Availability
NEWS LOGIN Welcome Banner and News Items
NEWS IPC8 For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that
specific topic.

All use of STN is subject to the provisions of the STN Customer
agreement. Please note that this agreement limits use to scientific
research. Use for software development or design or implementation
of commercial gateways or other similar uses is prohibited and may
result in loss of user privileges and other penalties.

* * * * * STN Columbus * * * * *

FILE 'HOME' ENTERED AT 04:02:48 ON 01 OCT 2008

=> index bioscience

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED

COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION

FULL ESTIMATED COST

0.21	0.21
------	------

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 04:03:14 ON 01 OCT 2008

69 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s biofilm and remov?(p)biofilm and protease and esterase and amylase and solut?
and alkaline and wash?

0* FILE ADISNEWS
0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
0* FILE CEABA-VTB
0* FILE CIN
0* FILE ESBIODASE

30 FILES SEARCHED...

0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA

```

1 FILE GENBANK
1 FILE IFIPAT
0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
60 FILES SEARCHED...
11 FILE USPATFULL
4 FILE USPAT2
0* FILE WATER

```

4 FILES HAVE ONE OR MORE ANSWERS, 69 FILES SEARCHED IN STNINDEX

L1 QUE BIOFILM AND REMOV?(P) BIOFILM AND PROTEASE AND ESTERASE AND AMYLASE AND SOLUT? AND ALKALINE AND WASH?

=> file genbank ifipat uspatfull uspat2
COST IN U.S. DOLLARS

SINCE FILE	TOTAL
ENTRY	SESSION
2.60	2.81

FULL ESTIMATED COST

FILE 'GENBANK' ENTERED AT 04:05:30 ON 01 OCT 2008

FILE 'IFIPAT' ENTERED AT 04:05:30 ON 01 OCT 2008
COPYRIGHT (C) 2008 IFI CLAIMS(R) Patent Services (IFI)

FILE 'USPATFULL' ENTERED AT 04:05:30 ON 01 OCT 2008
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'USPAT2' ENTERED AT 04:05:30 ON 01 OCT 2008
CA INDEXING COPYRIGHT (C) 2008 AMERICAN CHEMICAL SOCIETY (ACS)

=> s l1
L2 17 L1

=> dup rem l2
DUPLICATE IS NOT AVAILABLE IN 'GENBANK'.
ANSWERS FROM THESE FILES WILL BE CONSIDERED UNIQUE
PROCESSING COMPLETED FOR L2
L3 13 DUP REM L2 (4 DUPLICATES REMOVED)

=> d l3 1-13

```

L3 ANSWER 1 OF 13 USPATFULL on STN
AN 2008:29739 USPATFULL
TI Removable antimicrobial coating compositions and methods of use
IN Lu, Helen S.M., Wallingford, PA, UNITED STATES
Hoffmann, Christian, Newark, DE, UNITED STATES
Lenges, Christian Peter, Wilmington, DE, UNITED STATES
Stieglitz, Barry, Wynnewood, PA, UNITED STATES
Leger, Lynn, Mississauga, CANADA
VanGorp, Judith Johanna, Wilmington, DE, UNITED STATES
Malone, Shaun F., Ajax, CANADA
PI US 20080026026 A1 20080131
AI US 2007-710290 A1 20070223 (11)
PRAI US 2006-776081P 20060223 (60)
US 2006-831983P 20060719 (60)
DT Utility
FS APPLICATION
LN.CNT 2260
INCL INCLM: 424/405.000

```

INCLS: 422/028.000
NCL NCLM: 424/405.000
NCLS: 422/028.000
IC IPCI A01N0025-00 [I,A]; A01P0001-00 [I,A]; A61L0002-00 [I,A]
IPCR A01N0025-00 [I,C]; A01N0025-00 [I,A]; A01P0001-00 [I,C];
A01P0001-00 [I,A]; A61L0002-00 [I,C]; A61L0002-00 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 2 OF 13 USPATFULL on STN
AN 2007:314900 USPATFULL
TI Removable antimicrobial coating compositions and methods of use
IN Lu, Helen S.M., Wallingford, PA, UNITED STATES
Hoffmann, Christian, Newark, DE, UNITED STATES
Lenges, Christian Peter, Wilmington, DE, UNITED STATES
Leger, Lynn, Mississauga, CANADA
Malone, Shaun F., Ajax, CANADA
Stieglitz, Barry, Wynnewood, PA, UNITED STATES
Van Gorp, Judith Johanna, Wilmington, DE, UNITED STATES
PI US 20070275101 A1 20071129
AI US 2007-710325 A1 20070223 (11)
PRAI US 2006-776081P 20060223 (60)
US 2006-831983P 20060719 (60)
DT Utility
FS APPLICATION
LN.CNT 2259
INCL INCLM: 424/719.000
INCLS: 106/015.050; 514/642.000
NCL NCLM: 424/719.000
NCLS: 106/015.050; 514/642.000
IC IPCI A01N0033-12 [I,A]; A01N0033-00 [I,C*]; A01P0001-00 [I,A];
A01P0013-00 [I,A]; A01P0003-00 [I,A]
IPCR A01N0033-00 [I,C]; A01N0033-12 [I,A]; A01P0001-00 [I,C];
A01P0001-00 [I,A]; A01P0003-00 [I,C]; A01P0003-00 [I,A];
A01P0013-00 [I,C]; A01P0013-00 [I,A]
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 3 OF 13 IFIPAT COPYRIGHT 2008 IFI on STN
AN 10840879 IFIPAT;IFIUDB;IFICDB
TI Method of removing a biofilm; Washing
simultaneously or consecutively in solution comprising an
enzyme mixture containing at least one protease, at least one
esterase, and an amylase in a detergent with an
alkaline pH
IN Marion Karine
PA Unassigned Or Assigned To Individual (68000)
PPA karine Marion thierry Sanchez (Probable)
PI US 20050079594 A1 20050414
AI US 2003-695823 20031030
PRAI FR 2002-13963 20021031
US 2002-422508P 20021031 (Provisional)
FI US 20050079594 20050414
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
ED Entered STN: 19 Apr 2005
Last Updated on STN: 23 Aug 2007
CLMN 22

L3 ANSWER 4 OF 13 USPATFULL on STN
AN 2005:208966 USPATFULL
TI Protein variants having modified immunogenicity
IN Roggen, Erwin Ludo, Lyngby, DENMARK

Ernst, Steffen, Broenshoej, DENMARK
 Svendsen, Allan, Hoersholm, DENMARK
 Friis, Esben Peter, Valby, DENMARK
 Osten, Claus Von Der, Lyngby, DENMARK
 PA Novozymes A/S, Bagsvaerd, DENMARK (non-U.S. corporation)
 PI US 20050181446 A1 20050818
 AI US 2001-957806 A1 20010921 (9)
 PRAI WO 2001-DK293 20010430
 DK 2000-707 20000428
 DK 2001-327 20010228
 US 2000-203345P 20000510 (60)
 US 2001-277817P 20010321 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 12950
 INCL INCL: 435/007.100
 INCLS: 435/069.100; 435/320.100; 435/325.000; 702/019.000; 435/005.000
 NCL NCLM: 435/007.100
 NCLS: 435/005.000; 435/069.100; 435/226.000; 435/320.100; 435/325.000;
 506/014.000; 530/350.000; 702/019.000
 IC [7]
 ICM C12Q001-70
 ICS G01N033-53; G06F019-00; G01N033-48; G01N033-50; C12P021-02;
 C12N005-06
 IPCI C12Q0001-70 [ICM,7]; G01N0033-53 [ICS,7]; G06F0019-00 [ICS,7];
 G01N0033-48 [ICS,7]; G01N0033-50 [ICS,7]; C12P0021-02 [ICS,7];
 C12N0005-06 [ICS,7]
 IPCR A21D0002-00 [I,C*]; A21D0002-26 [I,A]; A21D0008-02 [I,C*];
 A21D0008-04 [I,A]; C07K0001-00 [I,C*]; C07K0001-04 [I,A];
 C07K0005-00 [I,C*]; C07K0005-103 [I,A]; C07K0005-11 [I,A];
 C07K0005-113 [I,A]; C07K0016-40 [I,C*]; C07K0016-40 [I,A];
 C11D0003-38 [I,C*]; C11D0003-386 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 5 OF 13 USPATFULL on STN
 AN 2005:104955 USPATFULL
 TI Multimolecular devices and drug delivery systems
 IN Cubicciotti, Roger S., Montclair, NJ, UNITED STATES
 PI US 20050089890 A1 20050428
 AI US 2004-872973 A1 20040621 (10)
 RLI Division of Ser. No. US 2001-907385, filed on 17 Jul 2001, GRANTED, Pat.
 No. US 6762025 Continuation of Ser. No. US 1998-81930, filed on 20 May
 1998, GRANTED, Pat. No. US 6287765
 DT Utility
 FS APPLICATION
 LN.CNT 15620
 INCL INCLM: 435/006.000
 INCLS: 530/395.000
 NCL NCLM: 435/006.000
 NCLS: 530/395.000
 IC [7]
 ICM C12Q001-68
 ICS C07K014-00
 IPCI C12Q0001-68 [ICM,7]; C07K0014-00 [ICS,7]
 IPCR C07H0021-00 [I,C*]; C07H0021-00 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 6 OF 13 USPATFULL on STN DUPLICATE 1
 AN 2004:144188 USPATFULL
 TI METHODS FOR ELIMINATING THE FORMATION OF BIOFILM
 IN Xu, Feng, Davis, CA, UNITED STATES
 PA Novozymes Biotech, Inc., Davis, CA, UNITED STATES, 95616 (U.S.)

corporation)

PI US 20040109852 A1 20040610
 US 6777223 B2 20040817

AI US 2001-885379 A1 20010619 (9)

RLI Continuation-in-part of Ser. No. US 2000-596795, filed on 19 Jun 2000,
 ABANDONED

DT Utility

FS APPLICATION

LN.CNT 995

INCL INCLM: 424/094.600
 INCLS: 424/094.200

NCL NCLM: 435/262.500; 424/094.600
 NCLS: 210/632.000; 424/094.100; 424/094.200; 435/189.000; 435/190.000

IC [7]
 ICM A61K038-54
 ICS A61K038-46
 IPCI A61K0038-54 [ICM,7]; A61K0038-46 [ICS,7]; A61K0038-43 [ICS,7,C*]
 IPCI-2 C12S0009-00 [ICM,7]; A61K0038-43 [ICS,7]
 IPCR A61L0002-18 [I,C*]; A61L0002-18 [I,A]; B08B0007-00 [I,C*];
 B08B0007-00 [I,A]; C02F0001-50 [I,C*]; C02F0001-50 [I,A];
 C12S0009-00 [I,C*]; C12S0009-00 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 7 OF 13 USPATFULL on STN DUPLICATE 2

AN 2003:37665 USPATFULL

TI Polypeptides having lactonohydrolase activity and nucleic acids encoding
 same

IN Berka, Randy M., Davis, CA, UNITED STATES
 Rey, Michael W., Davis, CA, UNITED STATES

PA Novozymes Biotech, Inc., Davis, CA, UNITED STATES, 95616 (U.S.
 corporation)

PI US 20030027310 A1 20030206
 US 6756220 B2 20040629

AI US 2002-126170 A1 20020419 (10)

RLI Division of Ser. No. US 1999-434690, filed on 5 Nov 1999, GRANTED, Pat.
 No. US 6395529 Continuation-in-part of Ser. No. US 1999-263041, filed on
 5 Mar 1999, ABANDONED Continuation-in-part of Ser. No. US 1998-189497,
 filed on 10 Nov 1998, ABANDONED

DT Utility

FS APPLICATION

LN.CNT 2289

INCL INCLM: 435/196.000
 INCLS: 435/069.100; 435/320.100; 435/325.000; 536/023.200

NCL NCLM: 435/197.000; 435/196.000
 NCLS: 435/252.300; 435/320.100; 435/929.000; 530/350.000; 536/023.200;
 435/069.100; 435/325.000

IC [7]
 ICM C12N009-16
 ICS C07H021-04; C12P021-02; C12N005-06
 IPCI C12N0009-16 [ICM,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0021-02 [ICS,7]; C12N0005-06 [ICS,7]
 IPCI-2 C12N0009-16 [ICM,7]; C12N0001-20 [ICS,7]; C12N0015-00 [ICS,7];
 C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
 IPCR C02F0001-50 [I,C*]; C02F0001-50 [I,A]; C12N0009-18 [I,C*];
 C12N0009-18 [I,A]

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 8 OF 13 USPATFULL on STN DUPLICATE 3

AN 2002:148647 USPATFULL

TI 2,6-beta-D-fructan hydrolase enzyme and processes for using the enzyme

IN Moller, Soren, Holte, DENMARK
 Johansen, Charlotte, Holte, DENMARK

Schafer, Thomas, Farum, DENMARK
 Ostergaard, Peter Rahbek, Virum, DENMARK
 Hoeck, Lisbeth Hedegaard, Skodsborg, DENMARK
 PA Novozymes A/S, Bagsvaerd, DENMARK, DK-2880 (non-U.S. corporation)
 PI US 20020076790 A1 20020620
 US 6524827 B2 20030225
 AI US 2001-969362 A1 20011002 (9)
 RLI Division of Ser. No. US 1999-397885, filed on 17 Sep 1999, GRANTED, Pat.
 No. US 6323007
 PRAI DK 1998-1173 19980918
 DK 1998-1623 19981209
 US 1998-101615P 19980924 (60)
 US 1998-111675P 19981210 (60)
 DT Utility
 FS APPLICATION
 LN.CNT 3312
 INCL INCLM: 435/200.000
 INCLS: 435/069.100; 435/325.000; 435/320.100; 435/101.000; 536/023.200
 NCL NCLM: 435/074.000; 435/200.000
 NCLS: 435/183.000; 435/252.300; 435/252.330; 435/320.100; 536/023.200;
 435/069.100; 435/101.000; 435/325.000
 IC [7]
 ICM C12P019-44
 ICS C07H021-04; C12N009-24; C12P021-02; C12N005-06
 IPCI C12P0019-44 [ICM,7]; C12P0019-00 [ICM,7,C*]; C07H0021-04 [ICS,7];
 C07H0021-00 [ICS,7,C*]; C12N0009-24 [ICS,7]; C12P0021-02 [ICS,7];
 C12N0005-06 [ICS,7]
 IPCI-2 C12N0009-24 [ICM,7]
 IPCR A61K0008-30 [I,C*]; A61K0008-64 [I,A]; A61K0008-66 [I,A];
 A61Q0011-00 [I,C*]; A61Q0011-00 [I,A]; A61Q0017-00 [I,C*];
 A61Q0017-00 [I,A]; C11D0003-38 [I,C*]; C11D0003-386 [I,A];
 C12N0009-24 [I,C*]; C12N0009-24 [I,A]; C12P0019-00 [I,C*];
 C12P0019-14 [I,A]; C12P0019-44 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 9 OF 13 USPATFULL on STN DUPLICATE 4
 AN 2002:60923 USPATFULL
 TI Single-molecule selection methods and compositions therefrom
 IN Cubicciotti, Roger S., Montclair, NJ, UNITED STATES
 PI US 20020034757 A1 20020321
 US 6762025 B2 20040713
 AI US 2001-907385 A1 20010717 (9)
 RLI Continuation of Ser. No. US 1998-81930, filed on 20 May 1998, GRANTED,
 Pat. No. US 6287765
 DT Utility
 FS APPLICATION
 LN.CNT 15716
 INCL INCLM: 435/006.000
 INCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300
 NCL NCLM: 435/006.000
 NCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300; 536/024.500
 IC [7]
 ICM C12Q001-68
 ICS C07H019-00; C07H021-00; C07H021-02; C07H021-04; C12P019-34
 IPCI C12Q0001-68 [ICM,7]; C07H0019-00 [ICS,7]; C07H0021-00 [ICS,7];
 C07H0021-02 [ICS,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*];
 C12P0019-34 [ICS,7]; C12P0019-00 [ICS,7,C*]
 IPCI-2 C12Q0001-68 [ICM,7]; C12P0019-34 [ICS,7]; C12P0019-00 [ICS,7,C*];
 C07H0021-02 [ICS,7]; C07H0021-00 [ICS,7,C*]
 IPCR C07H0021-00 [I,C*]; C07H0021-00 [I,A]
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 10 OF 13 USPATFULL on STN
 AN 2002:122473 USPATFULL
 TI Polypeptides having lactonohydrolase activity and nucleic acids encoding same
 IN Berka, Randy M., Davis, CA, United States
 Rey, Michael W., Davis, CA, United States
 PA Novozymes Biotech, Inc., Davis, CA, United States (U.S. corporation)
 PI US 6395529 B1 20020528
 AI US 1999-434690 19991105 (9)
 RLI Continuation-in-part of Ser. No. US 1999-263041, filed on 5 Mar 1999, now abandoned Continuation-in-part of Ser. No. US 1998-189497, filed on 10 Nov 1998, now abandoned
 DT Utility
 FS GRANTED
 LN.CNT 2055
 INCL INCLM: 435/197.000
 INCLS: 435/252.300; 435/320.100; 435/929.000; 536/023.200; 530/350.000
 NCL NCLM: 435/197.000
 NCLS: 435/252.300; 435/320.100; 435/929.000; 530/350.000; 536/023.200
 IC [7]
 ICM C12N009-16
 ICS C12N001-20; C12N015-00; C12N001-00; C07H021-04
 IPCI C12N0009-16 [ICM,7]; C12N0001-20 [ICS,7]; C12N0015-00 [ICS,7]; C12N0001-00 [ICS,7]; C07H0021-04 [ICS,7]; C07H0021-00 [ICS,7,C*]
 IPCR C02F0001-50 [I,C*]; C02F0001-50 [I,A]; C12N0009-18 [I,C*]; C12N0009-18 [I,A]
 EXF 435/197; 435/252.3; 435/320.1; 435/929; 536/23.2; 530/350
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 11 OF 13 USPATFULL on STN
 AN 2001:214863 USPATFULL
 TI 2,6- β -D-fructan hydrolase enzyme and processes for using the enzyme
 IN Moller, Soren, Holte, Denmark
 Johansen, Charlotte, Holte, Denmark
 Schafer, Thomas, Farum, Denmark
 Ostergaard, Peter Rahbek, Virum, Denmark
 Hoeck, Lisbeth Hedegaard, Skodsborg, Denmark
 PA Novozymes A/S, Bagsvaerd, Denmark (non-U.S. corporation)
 PI US 6323007 B1 20011127
 AI US 1999-397885 19990917 (9)
 PRAI DK 1998-1173 19980918
 DK 1998-1623 19981209
 US 1998-101615P 19980924 (60)
 US 1998-111675P 19981210 (60)
 DT Utility
 FS GRANTED
 LN.CNT 2422
 INCL INCLM: 435/074.000
 INCLS: 435/200.000; 435/252.330; 435/262.000; 435/274.000; 435/320.100
 NCL NCLM: 435/074.000
 NCLS: 435/200.000; 435/252.330; 435/262.000; 435/274.000; 435/320.100
 IC [7]
 ICM C12P019-44
 IPCI C12P0019-44 [ICM,7]; C12P0019-00 [ICM,7,C*]
 IPCR A61K0008-30 [I,C*]; A61K0008-64 [I,A]; A61K0008-66 [I,A]; A61Q0011-00 [I,C*]; A61Q0011-00 [I,A]; A61Q0017-00 [I,C*]; A61Q0017-00 [I,A]; C11D0003-38 [I,C*]; C11D0003-386 [I,A]; C12N0009-24 [I,C*]; C12N0009-24 [I,A]; C12P0019-00 [I,C*]; C12P0019-14 [I,A]; C12P0019-44 [I,A]
 EXF 536/23.1; 530/350; 435/183; 435/74; 435/200; 435/252.33; 435/262; 435/274; 435/320.1
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 12 OF 13 USPATFULL on STN
 AN 2001:152673 USPATFULL
 TI Methods for detecting and identifying single molecules
 IN Cubicciotti, Roger S., Montclair, NJ, United States
 PA Molecular Machines, Inc., Montclair, NJ, United States (U.S. corporation)
 PI US 6287765 B1 20010911
 AI US 1998-81930 19980520 (9)
 DT Utility
 FS GRANTED
 LN.CNT 15456
 INCL INCLM: 435/006.000
 INCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300; 536/024.500
 NCL NCLM: 435/006.000
 NCLS: 435/091.200; 536/022.100; 536/023.100; 536/024.300; 536/024.500; 977/853.000
 IC [7]
 ICM C12Q001-08
 ICS C12P019-34; C07M021-02
 IPCI C12Q0001-08 [ICM,7]; C12Q0001-06 [ICM,7,C*]; C12P0019-34 [ICS,7]; C12P0019-00 [ICS,7,C*]; C07M0021-02 [ICS,7]
 IPCR C07H0021-00 [I,A]; C07H0021-00 [I,C*]
 EXF 435/6; 435/91.2; 536/22.1; 536/23.1; 536/24.3; 536/24.5
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 13 OF 13 GENBANK® COPYRIGHT 2008 on STN

LOCUS (LOC): AE009952 GenBank (R)
 GenBank ACC. NO. (GBN): AE009952 AE013601-AE014015
 GenBank VERSION (VER): AE009952.1 GI:22002119
 SEQUENCE LENGTH (SQL): 4600755
 MOLECULE TYPE (CI): DNA; circular
 DIVISION CODE (CI): Bacteria
 DATE (DATE): 2 May 2006
 DEFINITION (DEF): *Yersinia pestis* KIM, complete genome.
 SOURCE: *Yersinia pestis* KIM
 ORGANISM (ORGN): *Yersinia pestis* KIM
 Bacteria; Proteobacteria; Gammaproteobacteria;
 Enterobacteriales; Enterobacteriaceae; *Yersinia*

COMMENT:

On or before May 2, 2006 this sequence version replaced
 gi:21956656, gi:21956667, gi:21956674, gi:21956680, gi:21956691,
 gi:21956705, gi:21956717, gi:21956732, gi:21956743, gi:21956757,
 gi:21956769, gi:21956778, gi:21956792, gi:21956799, gi:21956813,
 gi:21956829, gi:21956840, gi:21956852, gi:21956857, gi:21956868,
 gi:21956880, gi:21956892, gi:21956905, gi:21956914, gi:21956925,
 gi:21956938, gi:21956949, gi:21956964, gi:21956977, gi:21956986,
 gi:21956994, gi:21957003, gi:21957010, gi:21957020, gi:21957029,
 gi:21957037, gi:21957046, gi:21957059, gi:21957069, gi:21957080,
 gi:21957091, gi:21957100, gi:21957113, gi:21957124, gi:21957136,
 gi:21957145, gi:21957159, gi:21957165, gi:21957178, gi:21957184,
 gi:21957197, gi:21957202, gi:21957212, gi:21957224, gi:21957237,
 gi:21957247, gi:21957258, gi:21957269, gi:21957274, gi:21957284,
 gi:21957296, gi:21957307, gi:21957316, gi:21957328, gi:21957335,
 gi:21957345, gi:21957353, gi:21957368, gi:21957378, gi:21957392,
 gi:21957403, gi:21957413, gi:21957424, gi:21957437, gi:21957454,
 gi:21957462, gi:21957471, gi:21957482, gi:21957491, gi:21957497,
 gi:21957510, gi:21957522, gi:21957529, gi:21957541, gi:21957550,
 gi:21957562, gi:21957573, gi:21957582, gi:21957593, gi:21957603,
 gi:21957611, gi:21957622, gi:21957636, gi:21957648, gi:21957652,
 gi:21957662, gi:21957676, gi:21957683, gi:21957696, gi:21957703,

gi:21957715, gi:21957722, gi:21957732, gi:21957746, gi:21957761,
gi:21957770, gi:21957778, gi:21957788, gi:21957799, gi:21957814,
gi:21957826, gi:21957834, gi:21957843, gi:21957857, gi:21957872,
gi:21957884, gi:21957894, gi:21957899, gi:21957903, gi:21957915,
gi:21957932, gi:21957942, gi:21957954, gi:21957963, gi:21957971,
gi:21957982, gi:21957996, gi:21958007, gi:21958020, gi:21958030,
gi:21958045, gi:21958059, gi:21958071, gi:21958078, gi:21958087,
gi:21958099, gi:21958114, gi:21958120, gi:21958132, gi:21958147,
gi:21958153, gi:21958159, gi:21958170, gi:21958180, gi:21958192,
gi:21958205, gi:21958216, gi:21958225, gi:21958235, gi:21958249,
gi:21958258, gi:21958270, gi:21958281, gi:21958291, gi:21958305,
gi:21958314, gi:21958324, gi:21958333, gi:21958340, gi:21958354,
gi:21958367, gi:21958379, gi:21958388, gi:21958399, gi:21958412,
gi:21958422, gi:21958429, gi:21958438, gi:21958451, gi:21958463,
gi:21958475, gi:21958489, gi:21958495, gi:21958500, gi:21958514,
gi:21958526, gi:21958537, gi:21958551, gi:21958564, gi:21958575,
gi:21958589, gi:21958600, gi:21958612, gi:21958624, gi:21958631,
gi:21958640, gi:21958649, gi:21958661, gi:21958671, gi:21958680,
gi:21958691, gi:21958703, gi:21958716, gi:21958732, gi:21958744,
gi:21958752, gi:21958761, gi:21958770, gi:21958783, gi:21958794,
gi:21958803, gi:21958816, gi:21958827, gi:21958839, gi:21958850,
gi:21958861, gi:21958872, gi:21958884, gi:21958894, gi:21958906,
gi:21958917, gi:21958927, gi:21958936, gi:21958945, gi:21958955,
gi:21958965, gi:21958973, gi:21958983, gi:21958992, gi:21959005,
gi:21959014, gi:21959022, gi:21959031, gi:21959041, gi:21959057,
gi:21959073, gi:21959085, gi:21959096, gi:21959108, gi:21959117,
gi:21959127, gi:21959141, gi:21959154, gi:21959168, gi:21959177,
gi:21959190, gi:21959198, gi:21959206, gi:21959215, gi:21959227,
gi:21959235, gi:21959246, gi:21959257, gi:21959260, gi:21959263,
gi:21959274, gi:21959296, gi:21959307, gi:21959317, gi:21959327,
gi:21959338, gi:21959349, gi:21959364, gi:21959377, gi:21959389,
gi:21959401, gi:21959417, gi:21959427, gi:21959437, gi:21959453,
gi:21959463, gi:21959476, gi:21959488, gi:21959496, gi:21959508,
gi:21959515, gi:21959523, gi:21959533, gi:21959543, gi:21959554,
gi:21959567, gi:21959575, gi:21959584, gi:21959593, gi:21959605,
gi:21959617, gi:21959628, gi:21959640, gi:21959648, gi:21959659,
gi:21959670, gi:21959680, gi:21959688, gi:21959696, gi:21959711,
gi:21959720, gi:21959739, gi:21959751, gi:21959763, gi:21959774,
gi:21959782, gi:21959793, gi:21959805, gi:21959818, gi:21959832,
gi:21959847, gi:21959860, gi:21959874, gi:21959881, gi:21959890,
gi:21959899, gi:21959913, gi:21959925, gi:21959939, gi:21959948,
gi:21959961, gi:21959972, gi:21959984, gi:21959997, gi:21960007,
gi:21960019, gi:21960027, gi:21960042, gi:21960053, gi:21960065,
gi:21960078, gi:21960088, gi:21960093, gi:21960105, gi:21960115,
gi:21960129, gi:21960140, gi:21960147, gi:21960160, gi:21960168,
gi:21960177, gi:21960188, gi:21960202, gi:21960215, gi:21960228,
gi:21960237, gi:21960248, gi:21960255, gi:21960270, gi:21960277,
gi:21960291, gi:21960300, gi:21960309, gi:21960321, gi:21960333,
gi:21960343, gi:21960347, gi:21960356, gi:21960365, gi:21960376,
gi:21960382, gi:21960387, gi:21960399, gi:21960414, gi:21960424,
gi:21960435, gi:21960444, gi:21960456, gi:21960469, gi:21960480,
gi:21960490, gi:21960501, gi:21960520, gi:21960532, gi:21960540,
gi:21960548, gi:21960558, gi:21960569, gi:21960587, gi:21960597,
gi:21960608, gi:21960616, gi:21960625, gi:21960632, gi:21960645,
gi:21960654, gi:21960664, gi:21960673, gi:21960685, gi:21960695,
gi:21960707, gi:21960717, gi:21960725, gi:21960738, gi:21960747,
gi:21960761, gi:21960774, gi:21960789, gi:21960797, gi:21960806,
gi:21960814, gi:21960823, gi:21960833, gi:21960841, gi:21960851,
gi:21960862, gi:21960875, gi:21960881, gi:21960888, gi:21960899,
gi:21960910, gi:21960921, gi:21960933, gi:21960947, gi:21960955,
gi:21960971, gi:21960988, gi:21961004, gi:21961025, gi:21961042,
gi:21961051, gi:21961062, gi:21961073, gi:21961086, gi:21961093,

gi:21961103, gi:21961114, gi:21961127, gi:21961139, gi:21961149.

REFERENCE: 1 (bases 1 to 4600755)

AUTHOR (AU): Deng,W.; Burland,V.; Plunkett,G. III; Boutin,A.; Mayhew,G.F.; Liss,P.; Perna,N.T.; Rose,D.J.; Mau,B.; Zhou,S.; Schwartz,D.C.; Fetherston,J.D.; Lindler,L.E.; Brubaker,R.R.; Plana,G.V.; Straley,S.C.; McDonough,K.A.; Nilles,M.L.; Matson,J.S.; Blattner,F.R.; Perry,R.D.

TITLE (TI): Genome Sequence of Yersinia pestis KIM

JOURNAL (SO): J. Bacteriol., 184 (16), 4601-4611 (2002)

OTHER SOURCE (OS): CA 137:120475

REFERENCE: 2 (bases 1 to 4600755)

AUTHOR (AU): Deng,W.; Burland,V.; Plunkett,G. III; Boutin,A.; Mayhew,G.F.; Liss,P.; Perna,N.T.; Rose,D.J.; Mau,B.; Zhou,S.; Schwartz,D.C.; Fetherston,J.D.; Lindler,L.E.; Brubaker,R.R.; Plana,G.V.; Straley,S.C.; McDonough,K.A.; Nilles,M.L.; Matson,J.S.; Blattner,F.R.; Perry,R.D.

TITLE (TI): Direct Submission

JOURNAL (SO): Submitted (21-FEB-2002) Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

FEATURES (FEAT):

Feature Key	Location	Qualifier
source	1..4600755	/organism="Yersinia pestis KIM" /mol-type="genomic DNA" /strain="KIM" /db-xref="taxon:187410"
gene	complement(21..461)	/gene="mioC" /locus-tag="y0001"
CDS	complement(21..461)	/gene="mioC" /locus-tag="y0001" /function="factor; DNA - replication, repair, restriction/modification" /note="residues 1 to 146 of 146 are 67.12 pct identical to residues 1 to 146 of 147 from E. coli K12 : B3742; residues 1 to 146 of 146 are 68.49 pct identical to residues 1 to 146 of 147 from GenPept : >gb AAL22733.1 (AE008881) initiation of chromosome replication [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="initiation of chromosome replication" /protein-id="AAM83597.1" /db-xref="GI:21956657" /translation="MADITLISGSTLGSAEYVAE HLADKLEEAGFSTEILHGPELDEL TLNGLWLIVTSTHGAGDLPDNLQPLLEQIEQQKP DLSQVRFGAVGLGSSEYDTFCGAI IKLDQQLIAQGAQRLGEILEIDVIQHEIPEDPAE IWVKDWINLL"
gene	complement(554..1015)	/gene="asnC" /locus-tag="y0002"
CDS	complement(554..1015)	/gene="asnC" /locus-tag="y0002"

		/function="regulator; amino acid biosynthesis: Asparagine" /note="residues 3 to 153 of 153 are 84.76 pct identical to residues 2 to 152 of 152 from E. coli K12 : B3743; residues 3 to 153 of 153 are 86.09 pct identical to residues 2 to 152 of 152 from GenPept : >emb CAD03119.1 (AL627280) regulatory protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="regulator for asnA, asnC and gidA" /protein-id="AAM83598.1" /db-xref="GI:21956658" /translation="MSEIYQIDNLDRLSILKALME NARTPYAELAKNLAVSPGTIHVRV EKMRQAGIITAACVHVNPKQLGYDVCCFIGIILK SAKDYPSALKKLESLEEVVEAYYT TGHYSIFIKVMCKSIDALQQVLINKIQTIDEIQS TETLISLQNPIMRTIVP" /gene="asnA" /locus-tag="y0003" /gene="asnA" /locus-tag="y0003" /function="enzyme; amino acid biosynthesis: Asparagine" /note="residues 1 to 330 of 330 are 78.48 pct identical to residues 1 to 330 of 330 from E. coli K12 : B3744" /codon-start=1 /transl-table=11 /product="asparagine synthetase A" /protein-id="AAM83599.1" /db-xref="GI:21956659" /translation="MKKQFIQKQQQISFVKSFFS RQLEQQGLGIEVQAPILSRVGDGT QDNLSGSEKAVQVKVSLPDSTFEVVHSLAKWKR KTLGRFDFGADQGVYTHMKALRPD EDRLSAIHSVYVDQWDWERVMGDGERNLAYLKST VNKIYAAIKETEAASAEFGVKPF LPDHIQFIHSESLRARFPDLDAKGRERAIKELG AVFLIGIGGKLADGQSHDVRAPDY DDWTSPSAEGFSGLNQDIIVWNPILEDFAFEISSM GIRVDAEALKRQLALTGDEDRLEL EWHQSLLRGEMPQTIGGGIGQSRLVMLLLQKQHI GQVQCGVWGPEISEKVDGLL" /locus-tag="y0004" /locus-tag="y0004" /note="residues 57 to 488 of 488 are 65.04 pct identical to residues 1 to 427 of 427 from E. coli K12 : B3745; residues 1 to 488 of 488 are 64.34 pct identical to residues 1 to 483 of 483 from GenPept : >dbj BAB38110.1 (AP002566) hypothetical protein [Escherichia coli O157:H7]"
gene	1185..2177	
CDS	1185..2177	
gene	complement(2276..3742)	
CDS	complement(2276..3742)	

		/codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83600.1" /db-xref="GI:21956660" /translation="MLSLATLDMLLSISEGELIE EMVVGLLAAPQLAIFFEKFPRIKR ALMKDIPGWKQNLQQRIREASVPPGLANESLYQ QSLLEDSPQFYAHLDPDIVAQLQDL HSPFATQAKTLVQTADLAKNPPGGDSLQTLFLQR WRVSLILQTITIIHQLLQEREQL LAELQRRLLALSGALEPILTTNDNAAGRLWDMSQG HLQRGDYQLLLQYGDFLQQQPELI RLAEQLGRSRSKAQPAPDARYEPYTMVVRQPD VPEEVSGIHQSNLILRLPTLVM LGMSELEFEFYRRLLERRLLTYRLQGDNWQEK QRPVSLKQNDQPRGPFIVCVDT GSMGGFNEQCAKAFCLALLRIALADNRRCYIMLF ATEIIHYELSADNGIEQAIRFLNQ HFRGGTDLAACLANTLNKMEDREWYDADAVIISD FIAQRLPEELVRKIKIQQAQHR FHAVAMSAYGKPGIMRIFDHIWRFDTSLSRLIR RWKR"
gene	complement (3746..5299)	/locus-tag="y0005"
CDS	complement (3746..5299)	/locus-tag="y0005" /function="putative regulator" /note="residues 1 to 496 of 517 are 67.54 pct identical to residues 9 to 504 of 506 from E. coli K12 : B3746" /codon-start=1 /transl-table=11 /product="putative 2-component regulator" /protein-id="AAM83601.1" /db-xref="GI:21956661" /translation="MAQSSQLAERISRLSHALES GLYERQEAIRLCLLAALSGESVFL LGPPGIAKSLIARRLKFAFRHARAFEYLMTRFST PEEVFGPLSIQALKEEGRYQRMGTG GYLPEAEIVFLDEIWKAGPAILNTLLTAINERRF RNGDREDSIPMRLLVITASNELPDA DSSLEALYDRMLIRLWLDREVQEKQNFRLISRQ NENHNPVAENLSITDEEFHQWQPL IDKITLPDHCHELIFQLRQLSALEHAPYVSDRR WKKALRLQASAFFSGRDEITPID LILLKDCWLHDLNSFKLLQQQLEQLLTEQGYQQQ SLLMKLQDINSKWLQHQQQSDHQ ALTIVVKQSGMFSRKAQYALPDNLTDSTLTLLQK PLNLHDIQVNHQLQVDKEALAQWLN KGGALRAKLNGVGYAQSIDAEIDDQLHIIILDVS RQPSTLSLPGATTTVPPELLLAL TKLESTLAEQRRLFsqhQPClFTPSSWLAKIEAS LLQVVEQLQFQQIQFQQIQFQQRK FQQQKHSGH"
gene	5573..7441	/gene="kup"
CDS	5573..7441	/locus-tag="y0006" /gene="kup" /locus-tag="y0006" /function="transport; transport of small molecules; cations" /note="residues 1 to 505 of 622"

		are 83.96 pct identical to residues 1 to 505 of 519 from E. coli K12 : B3747; residues 1 to 622 of 622 are 84.72 pct identical to residues 1 to 622 of 622 from GenPept : >gb AAL22738.1 (AE008881) KUP family, potassium transport system, low affinity [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="low affinity potassium transport system" /protein-id="AAM83602.1" /db-xref="GI:21956662" /translation="MSTEHKQYLSAVTLAAIGVV YGDIGTSPLYTLRECFSGHYGFDV RPDVVFGFLSLIFWMLILVVSVKYLTYYMRADNA GEGGILTLMSLAGRNTSSRATSIL VVLGLIGGSFFYGEVVITPAISVMSAIEGLEIAA PALDPYIVPCSI AVLTL L FVIQKH GTG SVGKLFAPVMLVWFLTLALLGLRSIIANPEV LAALNPKWAISFFVEYKSVSFFAL GAVVLAITGVEALYADMGHFGKFP IRLAWFTVVL PSLV LNYFGQGALL LKNPEAIKNP FFLLAPDWALIPL LILATLATVIASQAVISGVFS LTRQAVRLGYLPPMRIIHTSEMES GQIYIPVINWTLYLAVVLVIIGFERSSNLAAAYG IAVTGTMVITSILFCTVAWKNWWH NRFLVVFLLMVLLIIDIPMFSANVLKLFSGGWLP LSLGLVMFIIMTTWKSERFSLLRR MHEHSNSLEAMIASLEKSPVVRVPGTAVYMSRAM NVIPFALLHNLKHNV LHERVVLL TMRTDDVPYVHNVERVTIEQLSPTFWRVVARYGW RETPNVAEIFHRCGLEGLSCQMME TSFFMSHESLILTKRPWHLFLRGKLFIALSRNAL RAPDQFEIPP NRVIELGTQVEI"
gene	7646..8065	/gene="rbsD" /locus-tag="y0007"
CDS	7646..8065	/gene="rbsD" /locus-tag="y0007" /function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="residues 1 to 139 of 139 are 68.34 pct identical to residues 13 to 151 of 151 from E. coli K12 : B3748" /codon-start=1 /transl-table=11 /product="D-ribose high-affinity transport system; membrane-associated protein" /protein-id="AAM83603.1" /db-xref="GI:21956663" /translation="MKKGVLNADISAVISRLGH TDQIVIGDAGLPIPATTTTRIDLAL TRGVPGFLQVVDVVTQEMQVENAYLAE EIVKNNP QLHEALLVLLTQLEQRQENQIALR YISHEAFKEQTKQSRVIRSGECSPFANIILGSG VTF"
gene	8116..9042	/gene="rbsK"

CDS	8116..9042	<pre> /locus-tag="y0008" /gene="rbsK" /locus-tag="y0008" /function="enzyme; degradation of small molecules; Carbon compounds" /note="residues 4 to 307 of 308 are 71.38 pct identical to residues 5 to 308 of 309 from E. coli K12 : B3752; residues 1 to 308 of 308 are 100.00 pct identical to residues 1 to 308 of 308 from GenPept : >emb CAC88875.1 (AJ414141) ribokinase [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="ribokinase" /protein-id="AAM83604.1" /db-xref="GI:21956664" /translation="METGKLVVLGSINADHILNI EQFPRPGETVIGQQYNVAFGGKGA NQAVAAGRSGADIAFIACVGDDDIGERVRRQLTA DKIDTQPIEAIKGATTGVALIFVN SDGENVIGINAGANSAVTPEYLRRYQQQVIDADA LLMQLESPLDTVIAAAKLAKQHQT QVILNPAPARKLPDELLTLVDMITPNETEAERLT GIHIEQDDDAKAAQILHDKGIAT VIITLGSRGVWLSEQGKGLVAGFKVNAVDTIAA GDTFNGALLTALLEGQSMDVAVRF AHAATAIAVTRPGAQPSIPWRAEIDSFLQERV" </pre>
gene	9062..9265	
CDS	9062..9265	<pre> /locus-tag="y0009" /locus-tag="y0009" /note="residues 6 to 46 of 67 are 56.09 pct identical to residues 194 to 234 of 330 from GenPept : >gb AAK16096.1 AF288084-2 (AF288084) NgrF [Phototribdus luminescens]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83605.1" /db-xref="GI:21956665" /translation="MSPVWQGYRQAMARAGLPPII AGYEVVSDFEFGGLVALKQRLNN PEAEPQVLPLTPELIERGSVSLR" </pre>
gene	complement(9262..10686)	
CDS	complement(9262..10686)	<pre> /locus-tag="y0010" /locus-tag="y0010" /function="putative transport" /note="residues 3 to 465 of 474 are 73.43 pct identical to residues 4 to 466 of 475 from E. coli K12 : B3754; residues 3 to 465 of 474 are 74.08 pct identical to residues 4 to 466 of 475 from GenPept : >gb AAL22745.1 (AE008881) putative MFS family transport protein (1st module) [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="putative permease" </pre>

```

/translation="MIKSARSMAGLPWIAAMAFF
MQALDATILNTALPSIAESLNRSP
LTMQSAIIISYTLTVAMLIPVSGWLADRFGTTRIF
ILAVSLFTFGSLLCALSGSLAFLV
ASRVIQGIGGAMMPVARLALIRAYPRSELLPVL
NFVTIPGLVGPVMSGPLLGGLLVTY
TTWHWIFILNIPIGLLGIFYARKYMPNFTMPKRT
FDFVGFLLFGISLVMISTSLLEIMG
RPEIADYLPAAATLLGGLLMLIFYIFHAKGHPNPL
IGLPLFKTRTFSVGIAGNVASRLG
TGCVPFLMPLMLQVGFYSGYALIAGCMMAPTAIGS
IMAKSAVTQVLRSLGYRKVLVGIT
LIIGVLIASFALQSPGMSAWMMILPLFILGIAMS
TQFTAMNTITLADLTDNNASSGNS
VLAVTQQLSISFGIAISATVLRFYDGLSLGGNVD
HFHYTFITMGIVTLLSSLVFLLLK
PRDGDNLIQGRNVKKVAPQVKNNV"

gene      complement(10766..11455 /locus-tag="y0011"
)
CDS       complement(10766..11455 /locus-tag="y0011"
)

/translation="MIKSARSMAGLPWIAAMAFF
MQALDATILNTALPSIAESLNRSP
LTMQSAIIISYTLTVAMLIPVSGWLADRFGTTRIF
ILAVSLFTFGSLLCALSGSLAFLV
ASRVIQGIGGAMMPVARLALIRAYPRSELLPVL
NFVTIPGLVGPVMSGPLLGGLLVTY
TTWHWIFILNIPIGLLGIFYARKYMPNFTMPKRT
FDFVGFLLFGISLVMISTSLLEIMG
RPEIADYLPAAATLLGGLLMLIFYIFHAKGHPNPL
IGLPLFKTRTFSVGIAGNVASRLG
TGCVPFLMPLMLQVGFYSGYALIAGCMMAPTAIGS
IMAKSAVTQVLRSLGYRKVLVGIT
LIIGVLIASFALQSPGMSAWMMILPLFILGIAMS
TQFTAMNTITLADLTDNNASSGNS
VLAVTQQLSISFGIAISATVLRFYDGLSLGGNVD
HFHYTFITMGIVTLLSSLVFLLLK
PRDGDNLIQGRNVKKVAPQVKNNV"

/locus-tag="y0011"
)
/locus-tag="y0011"
)

/note="residues 49 to 229 of 229
are 64.08 pct identical to
residues 1 to 180 of 181 from E.
coli K12 : B3755; residues 1 to
229 of 229 are 67.68 pct identical
to residues 1 to 229 of 230 from
GenPept :
>gb|AAG58958.1|AE005607-4
(AE005607) yieP gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83607.1"
/db-xref="GI:21956668"
/translation="MQLNTQQQAAQRNLSYLLAE
KIGQRILAGEYEAGSILPGEIELG
EQFGVSRITAVREAVKMLAAKGMLLPRPRIGTRVM
PQTNWNYLDQELLTWMMTKENFDQ
VMQHFLILRTSLEPQACYLAATHANEKQRELLAS
LVAEMRALHSNFNREQWIIQVDTQF
HKLIYEASGNPFLISFANLFSSVYYSYFRAITGD
EVIKLQHHQNIQVDTILAGDNQAL
FACQVLLKTVD"

gene      12016..13600 /locus-tag="yr001"
rRNA      12016..13600 /locus-tag="yr001"
/product="16S ribosomal RNA"

gene      13694..13766 /locus-tag="yt001"
tRNA      13694..13766 /locus-tag="yt001"
/product="tRNA-Glu"
/note="anticodon: TTC"

gene      14022..16928 /locus-tag="yr002"
rRNA      14022..16928 /locus-tag="yr002"
/product="23S ribosomal RNA"

gene      complement(17019..17426 /locus-tag="y0012"
)
CDS       complement(17019..17426 /locus-tag="y0012"
)

/note="residues 48 to 120 of 135

```


		are 30.00 pct identical to residues 84 to 159 of 443 from GenPept :
		>gb AAD36903.1 AE001821-3 (AE001821) hypothetical protein [Thermotoga maritima]"
		/codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83608.1" /db-xref="GI:21956669" /translation="MDGLSVYLIPGSVLLSHGET PHYHRRYGVSLSSAWGVGPPRY CRQVNSFLLLPNLIHVTGADTQSRTGDLTLTKGA LYQLSHISTTKFDAWQCPTLAWGD PTLPSALRRFTSEFGMGSGGTTALWPPGKFCFN"
gene	17036..17155	/locus-tag="yr003"
rRNA	17036..17155	/locus-tag="yr003" /product="5S ribosomal RNA"
gene	17169..17241	/locus-tag="yt002"
tRNA	17169..17241	/locus-tag="yt002" /product="tRNA-Thr" /note="anticodon: GGT"
gene	17285..17399	/locus-tag="yr004"
rRNA	17285..17399	/locus-tag="yr004" /product="5S ribosomal RNA"
gene	18140..19069	/gene="metA" /locus-tag="y0013"
CDS	18140..19069	/gene="metA" /locus-tag="y0013" /function="enzyme; amino acid biosynthesis: Methionine" /note="residues 1 to 309 of 309 are 79.61 pct identical to residues 1 to 309 of 309 from E. coli K12 : B4013; residues 1 to 309 of 309 are 79.61 pct identical to residues 1 to 309 of 309 from GenPept : >gb AAG59205.1 AE005633-2 (AE005633) homoserine transsuccinylase [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="homoserine transsuccinylase" /protein-id="AAM83609.1" /db-xref="GI:21956670" /translation="MPIRVPDELPAVSFLRNENV FVMASRAKTQEIRPLKVLILNLM PKKIETENQFLRLSNSPLQVDIQLLRVDSRESK NTPTEHLNNFYCDFEDIQDQNF LIVTGAPLGLVDFCDVAYWPQIERIIAWAKEHVT STLFVCWAVQAALNILYGIPKMTR EVKLSGIYQHQTLEPLALLTRGFDETFLAPHSRY ADFPVEVLQQYTDL DILVSSEEAG AYLFASKDKRVAFVTGHPEYDVDTLAGEYQRDLA AGLNPQVPLNYFPSDDASLRPKAS WRSHGHL LFANWLNYYVYQITPFDLRHMNPTLD"
gene	complement (19262..19411)	/locus-tag="y0014"

CDS	complement(19262..19411	/locus-tag="y0014"	
)		/note="residues 7 to 48 of 49 are 33.33 pct identical to residues 512 to 553 of 1005 from GenPept : >gb AAK39925.1 AF165818-133 (AF165818) hypothetical protein [Guillardia theta]"
			/codon-start=1
			/transl-table=11
			/product="hypothetical"
			/protein-id="AAM83610.1"
			/db-xref="GI:21956671"
			/translation="MSLPVKKAEFYGYFSPDRNK NNQLIHKIKNDFHFYGNIFLIFIY HIVNI"
gene	19456..21087		/gene="aceB"
			/locus-tag="y0015"
CDS	19456..21087		/gene="aceB"
			/locus-tag="y0015"
			/function="enzyme; central intermediary metabolism: Glyoxylate bypass"
			/note="residues 12 to 543 of 543 are 79.54 pct identical to residues 1 to 533 of 533 from E. coli K12 : B4014"
			/codon-start=1
			/transl-table=11
			/product="malate synthase A"
			/protein-id="AAM83611.1"
			/db-xref="GI:21956672"
			/translation="MAAVTLGRGIAMRQQLAGTE LVFTQPFNAAERQVLPDKAIEFLT ELVVKFSESRNQLLATRASWQQTIDQGALPDFIL ETNSIRDGDWKIQGIPADLRDRRV EITGPVERKMOVINALNANVKVFMADFEDSLAPSW DKVIDGQINLHDAVKGTISYTNES GKVYQLKPNPAVLIARVRGLHLPEKHVKWQDEAI PGGLDFDALYFYHNYQQLLAKGSG PYFYLPKMQSYQEAAWWSDFNFTEQRFGLSQGT IKATVLIETLPAVFQMDEILYHLR HHIVGLNCGRWDIYFSYIKTLKNHPDRVLPDRQS VTMNKPFLSAYSRLLIKTKHRGA LAMGGMAAFIPDKDAEKNKLVLDKVRADKELEAS NGHDTWVAHPGLADTVMDVFNKV LGSRPNQLEVSREQDKPITAAELLEPCSGERTEA GMRANIRVAVQYIEAWISGNGCVP IYGLMEDAATAEISRTSIWQWIHHQKSLSNGQTV TKELFRSMLSEEIQVVKLELGAER FDRGRFEEAARLMERITTQDELIDFLTLPGYALL A"
gene	21134..22441		/gene="aceA"
			/locus-tag="y0016"
CDS	21134..22441		/gene="aceA"
			/locus-tag="y0016"
			/function="enzyme; central intermediary metabolism: Glyoxylate bypass"
			/note="residues 4 to 435 of 435 are 85.18 pct identical to residues 3 to 434 of 434 from E. coli K12 : B4015; residues 1 to

gene 22514..24241

CDS 22514..24241

435 of 435 are 100.00 pct
identical to residues 1 to 435 of
435 from GenPept :
>emb|CAC93193.1| (AJ414158)
isocitrate lyase [Yersinia
pestis]"
/codon-start=1
/transl-table=11
/product="isocitrate lyase"
/protein-id="AAM83612.1"
/db-xref="GI:21956673"
/translation="MTISRTQQIQQLEQEWTS
PRWKNITRPYSAEDVIKLRGSVNPEC
TFAQNGAKKLWELLHGGSRKGYINCLGALTGGQA
LQQAAGVEAIYMSGWQVAADANT
ASSMPDQSLYPVDSVPAVVKRINNSFRRADQIQ
WSNNIEPGSKGYTDYFLPIVADAE
AGFGGVLNAFELMKAMIEAGAAGVHFEDQLAAVK
KCGHMGKVLVPTQEAIQKLVAAR
LAADV LGVPTLLIARTDADAADLLTSDCDPYDRE
FITGDRTAEGFFRTRAGIEQAISR
GLAYAPYADLVWCETSTPDLALAKRFADAVHAQF
PGKLLAYNCSPSFNWKKNLTDQQI
ASFQDELSAMGYKYQFITLAGIHSMWFNMFDLAH
AYAQQEGMKHYVEKVQQPEFASVD
RGYTFASHQQEVEGTGYFDKVTNIIQGGASSVTAL
TGSTEEQQF"
/gene="aceK"
/locus-tag="y0018"
/gene="aceK"
/locus-tag="y0018"
/function="enzyme; central
intermediary metabolism:
Glyoxylate bypass"
/note="residues 5 to 572 of 575
are 75.52 pct identical to
residues 5 to 572 of 578 from E.
coli K12 : B4016; residues 5 to
572 of 575 are 75.88 pct identical
to residues 5 to 572 of 578 from
GenPept :
>gb|AAG59208.1|AE005633-5
(AE005633) isocitrate
dehydrogenase kinase/phosphatase
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="isocitrate dehydrogenase
kinase/phosphatase"
/protein-id="AAM83613.1"
/db-xref="GI:21956675"
/translation="MVAKLEQLIAQTILQGFDQA
YGRFLEV TAGAQHRFEQADWHAVQ
QAMKKRIHLYDHHVGLVVEQLKYITDQRHFDVEF
LARVKEIYTGLLPDYPRFEIAESF
FNSVYCRLFKHRDLTPDKL FVFSSQPERRFREIP
RPLARDFIPKGDLSGMLQMVNLNDL
SLRLHWENLSRDIDYIVMAIRQAFTDEQLASAHF
QIANELFYRNKAAWLVGKLRLNGD
IYPFLLP IHHNESGELFIDTCLTSKAEASIVFGF
ARSYFMVYVPLPAAMVEWLREILP
GKSTAELYTAIGCQKHGKTESYREYLAFIHQSSE

```

QFIIAPGVKGMVMLVFTLPSFDRV
FKVIKDQFAPQKEVTQARVLECYQLVKEHDRVGR
MADTQEYENFVIDKHRISPELLAE
LQHEVPEKLEDLGDKIVIKHLYMERRMTPLNLYM
EQADDQQLKDAIEEYGNAIKQLAA
ANIFPGDMLFKNFGVTRHGRVVFYDYDEICYMTE
VNFRDIPPPRYPEDEMASEPWYSV
SPNDVFPFEEFRHFLCSDRKVRHFFFEEMHGDLFQA
SYWRGLQQRIRDGHVEDVFAYRRK
QRFSQRALN"
gene      complement(24077..24214 /locus-tag="y0017"
)
CDS       complement(24077..24214 /locus-tag="y0017"
)
          /note="residues 1 to 39 of 45 are
          35.89 pct identical to residues
          160 to 198 of 460 from GenPept :
          >gb|AAF52902.1| (AE003628) CG13138
          gene product [Drosophila
          melanogaster]"
          /codon-start=1
          /transl-table=11
          /product="hypothetical"
          /protein-id="AAM83614.1"
          /db-xref="GI:21956676"
          /translation="MLSSISKNILHMPIDTLLQ
          AAPITGLEQIAVHLLKKVPDFPVT A"
gene      complement(24361..24954 /gene="iclR"
)
          /locus-tag="y0019"
CDS       complement(24361..24954 /gene="iclR"
)
          /locus-tag="y0019"
          /function="regulator; central
          intermediary metabolism:
          Glyoxylate bypass"
          /note="residues 5 to 192 of 197
          are 78.19 pct identical to
          residues 98 to 285 of 287 from E.
          coli K12 : B4018"
          /codon-start=1
          /transl-table=11
          /product="repressor of aceBA
          operon"
          /protein-id="AAM83615.1"
          /db-xref="GI:21956677"
          /translation="MDHGGPHAFIVGSSFLQSRN
          LLAMVHPMLRRLMDESGETVNLAV
          LDHSDYQAI IIDQVQCTALMRMSAPIGGKLPMAH
          SGAGKAFLSTLPDDQLVQLLHKKG
          LHAYTQHTRTNPTSLKENLALIRKQGYSFDEEH
          ALGLRCIAACLFDEHHEAFAAISI
          SGPISRITDDRVTTEL GALVIHAAKEITQSYGGGT
          GVK"
gene      25420..29115      /gene="meth"
          /locus-tag="y0020"
CDS       25420..29115      /gene="meth"
          /locus-tag="y0020"
          /function="enzyme; amino acid
          biosynthesis: Methionine"
          /note="residues 6 to 1231 of 1231
          are 85.90 pct identical to

```

residues 1 to 1227 of 1227 from E.
coli K12 : B4019; residues 6 to
1231 of 1231 are 86.14 pct
identical to residues 30 to 1256
of 1256 from GenPept :
>gb|AAL23012.1| (AE008895)
B12-dependent
homocysteine-N5-methyltetrahydrofo
late transmethyrase, repressor of
metE and metF [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="B12-dependent
homocysteine-N5-methyltetrahydrofo
late transmethyrase, repressor of
metE and metF"
/protein-id="AAM83616.1"
/db-xref="GI:21956678"
/translation="MVDTVIDNKKVLEHQQLAQR
ILVLDGGMGTMIQSYRLEEADYRG
ARFADWASDLKGNNDLLVLSKPEVITAIHNAYLE
AGADILETNTFNSTSIAMADYQMA
SLSAEINYEAAARLARICADEWSARTPEKPRYVAG
VLGPTNRTASISPKVNDPAFRNVS
FDQLVEAYRESTRALIEGGVDLIMIETVFDTLNA
KAATFAVESEFEVMGVLLPVMISG
TITDASGRTLSGQTTEAFYNLSLRHVKPLSFGLNC
ALGPDELRLQYVAELSRISEYYVSA
HPNAGLPNAFGEYDLEAKEMAEQIGEWARAGFLN
IVGGCCGTTPRHIAAMVNAVAGVP
PRPLPDIPVACRLAGLEPLTIDANTLFVNVGERT
NVTGSARFKRLIKEEKGALDVA
RQQVESGAQIIDINMDEGMLDAEAAMVRFLNLIA
GEPDIARVPIMIDSSRWDVIEKGL
KCIQKGIVNSISMKEGVDAFIHHAKLVRRYGAA
MVMMAFDETGQADTRARKIEICRR
AYKILTETVGFPPEDIIFDPNIFAVATGIEEHNN
YAVDFIEACADIKAEPLHALISGG
VSNVSFSFRGNPVRFAIHAVFLYYAIRNGMDMG
IVNAGQLAIYDDLDELDAVEDV
ILNRRDDSTERLLDLAEKYRDSKSGEVAIQQA
RGWPVVKRLEYSLVKGITEFIELD
TEEARQQADRPVIEGPLMSGMNVVGDLFGEGK
MFLPQVVK SARVMKQAVAYLEPYI
EASKQKGT TAGKILLATVKGDVHDIGKNIVGVVL
QCNNEYIIDLGMVPTKILRTAR
EEKVDIIIGLSGLITPSLDEMNVVAKEMERQGF
TLLIGGATT SKAHTAVKIEQNYSG
STTYVSNASRSGVVSALLSDTQREAFVAKTRKE
YETVRIQHARKKPRTPPVSLQAAR
NNPTVIDWENYTPPAHKLGVQVVEASIE
TLRNYIDWTPFFMTWSLAGKYPRILEDEV
VGEEAKRLLADANALLDKLSAEDLLHPKGVVGLF
PANSVGDDIEIYRDERRDEVLAIS
YHLRQQTEKTD FPNYCLADYVAPKSSGKADYFGA
FAVTGGLEEDALADAYDAQHDDYN
KIMIKALSDRLAEAFAYLHERVRKVYWG
FAPNELSNEELVRENYQGIRPAPGY
PACPEHTEKGQIWQLLDVETHTGMKLT
ESYAMWPGASVSGWYF SHPDSKYFAVAQ
IQRDQVEDYAARKGMPTAEVERW
LAPNLGYDAD"

```

gene      complement(29211..34175 /gene="hylA"
)
CDS       complement(29211..34175 /gene="hylA"
)
          /locus-tag="y0021"
          /function="putative factor;
          extracellular functions; secreted
          proteins"
          /note="residues 20 to 1651 of 1654
          are 42.08 pct identical to
          residues 1 to 1604 of 1608 from
          GenPept : >gb|AAA50323.1| (M22618)
          hemolysin [Serratia marcescens]"
          /codon-start=1
          /transl-table=11
          /product="hemolysin precursor"
          /protein-id="AAM83617.1"
          /db-xref="GI:21956679"
          /translation="MRTPCYSYQEISPQNGDVKM
          KKHTFKLSPAGKLAAVTIISVSV
          ATCYAAGIVGAGDSAHKPDVSSVNGTSVINIVQP
          SASGLSHNQFQDFNVGEKGAVLNN
          ATSAGNSILAGQLAANQNNGQAASIILNEVISR
          NPSLLLGQQEIFGMTADYILANPN
          GITCNGCGFMNTNRESLVVGNPLIEQGLKGFET
          FNNNNWLI IQDKGLTANKILDLIA
          PRIEVTGMVTSTEAINALSGNNQISTDQILES R
          QEDHPNRPTSLGGWFSSLFSSSESE
          ESIDGKYLGSMSQGRINLVSTREGSGVKIAGSLN
          GSEEINATIKGKLQLEAAKLGGND
          ININANSIQAFGNLHKNE DNGGVTQSLERTQLKG
          KNIAIVANKKNQLSAVKIDADNVT
          LRGGELVLDERILTKTEQESSDGGNGVLGLGKW
          NWSENKEEKQQTSIGTTITAKNNA
          SLESTQDDIKLSAATITAGKNLAIAKAKDLHIDG
          AIEENSIHDYGHNYKHMVKDESWN
          NKTTKQTLNKTTLEAGKNLGLTAENKITTQGIKA
          SAGGDVVIDANDVKIGVQKTSNQE
          TTDGKHERNLGLGGVDHNNNDKYAETSHSSEITA
          DGNILISVKDDVAITGSKVKATKD
          GFVQAKEGGIKIDNAISTTTNKVDERTGVAFDIT
          GSSKKANNSEEKSTGSEVVSEANL
          KII SKKDVDVIGSLVK SAGELGIETLGDINVAAA
          QEKQKIDEQKTLTIDGFTSDDGK
          NQYQAGLKVEHTSESEKTEKVINHGSTLEGGTVK
          LEADKDVTF TGSQ LNTTKGDADIT
          AENVSFVAAQDTTTSNKEKETVGVNAHYTGMDK
          AGSGAGVSYEETKTDSEKSTAVVS
          HTDVKGDLNLNAKQEITNQGTDHNVEGSYAANAT
          NVNNLAAENSETTTTTTNTVDVKY
          GGNIA YDGVTRPVEKTIESGKKLDVGGVIENVG N
          VAPDSVNAGVDLSVNVGEKENKSS
          NSQAVVTSIKSGDISITAKEDVKDQGTHYQADKG
          GIKIDAANHTFESAVNRAEESEKV
          VSGGVDMRIYTTTGEDINVDAGKGGENKQQEVKA
          EQAQTGSMKAVGDIIINVQENARY
          QGTDLD SGDGKIAITAGEEIKFEQATSHLSEHNH N
          KIDANAKANFGTKPNSKDFGGGLG
          GGHSQGSTSADIAQVSHLHGKQGIELNAGKDLTL
          QGTEFGSKNAATGDVQLTAGGKVD
          FQAAQSQSSKQDMTWSASVKAGKSKSNSTSENDD

```

GTKTHTNKGF SAGAEANVKNTDE
 TSLTHQGGI INSN GAVTIKADGKDQQAIHLQNTN
 IISQETILNADNGGIVMESAQDKE
 HKNNWNVNTNLNGSQKNTIKSDDQGVVDKDSAKK
 IHNAAIKLDGGVDKLD SVTQQNTH
 INSDKVTLNSAKNTELAGAVLQANQISGQIGGDL
 NVISRENRLNKVNVSAALGGSHSN
 AKQDSLISQVANASPIMSDKIKNKL
 EEKSTKIFDKVENKFNTLGKEKDDSVQTISYTK
 DGQTVKISEADEKKETKDKWWQKGAKSVGKKIKS
 AVQDEQVVGGNGSVKANVEEVESQ
 GVEEQSAIRGTQNVDLTVKGKTDLVGGKISSKNS
 DVKLKTNGLETQDINGKYTEGGAR
 LNASSVMDMISDGAKDVMGKAPLVSGHGKSEQ
 KNATGGITRE"

gene complement(34188..35964 /locus-tag="y0022"
)

/note="hylB; disrupted by
 frameshift"
 /pseudo

gene complement(36445..37830 /gene="lysC"
)

CDS complement(36445..37830 /locus-tag="y0023"
 /gene="lysC"
)

/locus-tag="y0023"
 /function="enzyme; amino acid
 biosynthesis: Lysine"
 /note="residues 14 to 461
 are 81.47 pct identical to
 residues 2 to 449 of 449 from E.
 coli K12 : B4024; residues 14 to
 461 of 461 are 81.47 pct identical
 to residues 2 to 449 of 449 from
 GenPept :
 >gb|AAG59223.1|AE005635-3
 (AE005635) aspartokinase III,
 lysine sensitive [Escherichia coli
 O157:H7 EDL933]"
 /codon-start=1
 /transl-table=11
 /product="aspartokinase III,
 lysine sensitive"
 /protein-id="AAM83618.1"
 /db-xref="GI:21956681"
 /translation="MIQVAPQQTRDAPSATVVAK
 FGGTSVASFDAMSR SADVVLSNP
 VRLVILSASAGITNLLVALADGSEPEKRA
 DHDLED
 IRHIQYDIIARLTDSTVIREEIDR
 MLENIAMLSEAASLATSPALTDLVSHGELM
 STL
 LFVELLRQRQVAVVEWFDVRKVMRT
 NDRFGRAEPDTSALAELAQTLLAPRIE
 DAIVVTQ
 GFIGSEGKGRITTLGRGGS DYTA
 A
 LLGEALNVSRI DIWTDVPGIYTTDPRV
 VPAAKRI
 DKIAFEEAAEMATFGAKILHPATL
 LPAVRSDIPMFVGSSKDP AAGGTLVCNE
 TYNPPL
 FRALALRRKQTLLTLHSLNMLHAR
 GFLAEVFNILARHSISVDLITTSEVSVAL
 TLDTT
 GSTSTGDSLLTTSLLTELSSL CRV
 EVEEDLALVAIIGNNLSQACGVGKEVFGV
 LDPFN
 IRMICYGASSHNLCFLVPGNDADK
 VVQTLHYNLFE"

gene	38200..39846	/gene="pgi"
		/locus-tag="y0024"
CDS	38200..39846	/gene="pgi"
		/locus-tag="y0024"
		/function="enzyme; energy metabolism, carbon: Glycolysis"
		/note="residues 1 to 548 of 548 are 87.40 pct identical to residues 1 to 548 of 549 from E. coli K12 : B4025; residues 1 to 548 of 548 are 87.40 pct identical to residues 1 to 548 of 549 from GenPept : >gb AAG59224.1 AE005635-4 (AE005635) glucosephosphate isomerase [Escherichia coli O157:H7 EDL933]"
		/codon-start=1
		/transl-table=11
		/product="glucosephosphate isomerase"
		/protein-id="AAM83619.1"
		/db-xref="GI:21956682"
		/translation="MKNINPSQTAAWKALQQHFE QMKDVTISSLFAKDDQRFNRFSAT FDDQMLVDFSKNRITSETLEKLQDLAKETDLAGA IKSMFSGEKKINRTEDRAVLHIALR NRSNTPIVVDGKDVMEVNAVLAQMKQFCDRVIS GDWKGYTGKAITDVVNIGIGGSDL GPYMVTEALRPYKNHLMHFVSNVDGTHIAEALK PLNPETTFLVASKTFTTQETMTN AHSARDWFLSAAGDPAHVAKHFAALSTNAKAVGE FGIDTNNMFEFWDWVGGRYSLWSA IGLSIALSVGFHFEQLLSGAHAMDKHFAETPAE KNLPVLLALIGIWINNFFGAETEA ILPYDQYMHFRFPAYFQQGNMESNGKYVDRNGHPV DYQTGPPIIWGEPGTNGQHAFYQLI HQGTKLIPCDFIAPAISHNPLSDHHAKLLSNFFA QTEALAFGKSLEDVEAEFAAAGKT PEQVAHVAPFKVFEGNRPTNSILLREITPFSLGA LIALYEHKIFTQGVILNIYTFDQW GVELGKQLANRILPELADDQEVTSKDSSTNALIN RFKNWR"
gene	39981..40388	/locus-tag="y0025"
CDS	39981..40388	/locus-tag="y0025"
		/note="residues 6 to 135 of 135 are 67.69 pct identical to residues 8 to 136 of 136 from E. coli K12 : B4030"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83620.1"
		/db-xref="GI:21956683"
		/translation="MAKNRSQWIAKNLQRLNVL GLIMLAAILVVFLVKETIHLGKVL FLSNQETSSYMLIEGIVIIYFLYFEFIALIVKYFE SGYHFPLRYFIYIGITAIIRLIIV DHENPIDTLIYSGSILVLVVTLYLANTERLKRE"
gene	complement(40531..41442)	/gene="malG"
)	/locus-tag="y0026"


```

CDS      complement(40531..41442 /gene="malG"
)
        /locus-tag="y0026"
        /function="transport; transport of
        small molecules; carbohydrates,
        organic acids, alcohols"
        /note="residues 8 to 303 of 303
        are 88.17 pct identical to
        residues 1 to 296 of 296 from E.
        coli K12 : B4032; residues 8 to
        303 of 303 are 90.87 pct identical
        to residues 1 to 296 of 296 from
        GenPept : >gb|AAL23051.1|
        (AE008897) ABC superfamily
        (membrane), maltose transport
        protein [Salmonella typhimurium
        LT2]"
        /codon-start=1
        /transl-table=11
        /product="inner membrane permease
        of maltose/maltodextran ABC
        transporter"
        /protein-id="AAM83621.1"
        /db-xref="GI:21956684"
        /translation="MTKEEMQMAMVQPKSQRLRL
        LGTHFLMLCFIALIMFLLMVIAI
        SLRPGNFATGSLIPDQISWEHWKLALGMSVTHAD
        GSVTPPPFPVMLWLWNSIKIALIT
        AMGIVALSTTCAYAFARMRFRGKSALLKGMLIFQ
        MFPAVLSLVALYALFDRIGQYMPF
        IGLNTHGGVIFAYMGGIALHVWTIKGYFETIDNS
        LEEAAALDGATPWQAFRLVLLPLS
        VPILAVVFILSFIAAITEVPVASLLLRDVNSYTL
        AVGMQQYLNPQNYLWGDFAAAVL
        SAIPITTVFLLAQRWLVGGLTAGGVKG"

gene      complement(41435..43027 /gene="malF"
)
        /locus-tag="y0027"

CDS      complement(41435..43027 /gene="malF"
)
        /locus-tag="y0027"
        /function="transport; transport of
        small molecules; carbohydrates,
        organic acids, alcohols"
        /note="residues 18 to 530 of 530
        are 75.43 pct identical to
        residues 5 to 514 of 514 from E.
        coli K12 : B4033"
        /codon-start=1
        /transl-table=11
        /product="inner membrane permease
        of maltose ABC transporter"
        /protein-id="AAM83622.1"
        /db-xref="GI:21956685"
        /translation="MKGNIMQLSHTELQSRKKKI
        AWWQSDALKWLVISLLSLFTCYLI
        VLMYAQGEYLFIAIVTLILVSLGLYVFANRRAYAW
        RYVYPGVAGMGLFVLFPLICTIAI
        AFTNYSSTNQLTFERAQSVLLDRQFQTGKTFTFG
        LYPQSDNQWRLQLTNPDDGSLFISE
        PFSFEATGEQKVMVAPTNTAQTSEPASLRIITQS
        RQALSSLVAILPDGAELRMSSLRQ

```

```

FSGTKPLYTLGADGKELINQQTGVKYWPNPSTGF
YQAVNADGQWENEKLSPGFTVSIG
WKNFLRVLHDEGIQKPFISIFIWTILFSVMSVTF
TVAVGMVLACVVQWDSLKGKAIYR
VMLILPYAVPSFISILIFKGLFNQSFGEINLMLS
HLFGIKPAWFSDPITAKSMILIVN
TWLGYPYMMILCMGLLKAIPDDLYEASAMDGAGP
FQNFFRITFPLLIKPLTPLMIASF
AFNFNNFVLIQLLTNGGPDMMIGTSTPAGYTDLLV
NYTYRVAFEFEGGQDFGLAAAIAT
LIFILVGALAILNLKASKMNFN"
gene      complement(43199..44410 /gene="maleE"
)
/locus-tag="y0028"
CDS      complement(43199..44410 /gene="maleE"
)
/locus-tag="y0028"
/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="substrate recognition for
ABC transporter and chemotaxis;
residues 14 to 403 of 403 are
84.61 pct identical to residues 7
to 396 of 396 from E. coli K12 :
B4034; residues 7 to 403 of 403
are 84.13 pct identical to
residues 4 to 396 of 396 from
GenPept : >emb|CAD09213.1|
(AL627282) periplasmic
maltose-binding protein
[Salmonella enterica subsp.
enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="periplasmic
maltose-binding protein"
/protein-id="AAM83623.1"
/db-xref="GI:21956686"
/translation="MTRSFTKSGIGKTARVLALS
ALTTLVLSSSAFAKIEEGKLVIWI
NGDKGYNGLAEVGKKFEKDTGIKVTIEHPDKLEE
KFPQVAATGDGPDIIIFWAHDRFGG
YAQSGLLAELTPSKAFQEKLFPTWDAVRFNGKL
IGYPVAVEALSLIYNKDLVKEAPK
TWEEIPALDKTLRANGKSAIMWNLQEPYFTWPVI
AADGGYAFKFENGVDYDAKNVGVNN
AGAQAQLQFIVDLVKNKHINADTDYSIAEAAFNK
GETAMTINGPWAWSNIDKSKINYG
VTLLPTFHGQPSKPFVGVLTAGINAASPNKELAT
EFLENYLITDQGLAEVNKDKPLGA
VALKSFQEQLAKDPRIAATMDNATNGEIMPNIPO
MAAFWYATRS AVLNAITGRQTVEA
ALNDAATRITK"
gene      44888..45250 /locus-tag="y0030"
CDS      44888..45250 /locus-tag="y0030"
/note="residues 9 to 49 of 120 are
36.58 pct identical to residues 24
to 64 of 604 from GenPept :
>gb|AAK27723.1|AF358444-1
(AF358444) alpha-glucosidase
[Bifidobacterium adolescentis]"

```

		/codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83624.1" /db-xref="GI:21956687" /translation="MLSARSIPNPALYRIHPVSF RDGQGNVGVDYRGLNGVCDLLPC WISMLRRCSTCSPILRPRRRPGQPCHWLGGTARS ERVIRALGVINGSCRGLLPLFFFI QIHMKSLRKQRSNAWLM" /locus-tag="y0029" /locus-tag="y0029" /note="residues 33 to 76 of 78 are 34.78 pct identical to residues 399 to 444 of 933 from GenPept : >gb AAG51093.1 AC025295-1 (AC025295) auxin response factor 6 (ARF6) [Arabidopsis thaliana]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83625.1" /db-xref="GI:21956688" /translation="MRLIITLLDQYVEALFNVQP YTQAATPSGATLPLAWRHGAQRES HQGTGGNQWVMPGFASTVFLHSDSYEKLFQAQAKE "
gene	44998..45234	
CDS	44998..45234	
		/gene="malK" /locus-tag="y0031" /gene="malK" /locus-tag="y0031" /function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="residues 1 to 369 of 369 are 84.90 pct identical to residues 1 to 371 of 371 from E. coli K12 : B4035; residues 1 to 369 of 369 are 84.55 pct identical to residues 1 to 369 of 369 from GenPept : >gb AAL23054.1 (AE008897) bifunctional: ABC superfamily (atp-bind), maltose transportprotein; phenotypic repressor of mal operon [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="ATP-binding component of ABC transport system for maltose" /protein-id="AAM83626.1" /db-xref="GI:21956689" /translation="MANVTLSVYKAFGEAVISR DINLEIDDGEFVVFVGPSCGKST LLRMIAGLEDITSGELLIGGKRMNEVPPSERGIG MVFQSYALYPHLSVAENMSFGLKL AGVKKAEIYQRVNQVAEVLQLAHLLDRRPKALSG GQRQ RVAIGRTL VSEPDVFLLEP LSNLD AALRVQMRIEISRLHKRLERTMIYVTHDQ VEAMTLADKIVVLDAGNIAQVGKP LELYHYPANRFVAGFIGSPKMNFLPVKVTA AEPR QVQIELPNHQRVWLPVEGDQVQVG
gene	45238..46347	
CDS	45238..46347	

		ANMSLGIRPEHLLPSSASEVTLEGEIQVVEQLGN ETQIHQIPAIRQNLVYRQNDVVL VEEGATFSIGLPPHRCFLFREDGTACKRLYQELG V"
gene	46250..47689	/gene="lamB" /locus-tag="y0032"
CDS	46250..47689	/gene="lamB" /locus-tag="y0032" /function="transport of small molecules; carbohydrates, organic acids, alcohols" /note="defective for phage lambda uptake; residues 83 to 475 of 479 are 87.96 pct identical to residues 2 to 400 of 400 from GenPept : >gb AAA70348.1 (U16150) maltoporin [Yersinia enterocolitica]" /codon-start=1 /transl-table=11 /product="maltose high-affinity receptor" /protein-id="AAM83627.1" /db-xref="GI:21956690" /translation="MQHSPSVCHRIGVTSSVRMA LHVSGCTKNWASSYGDOWLQRMKA RMPTGKYNRRLMITLRKLPALAVAAGVLSTQA MAVDFHGYARSGIGWTASGGEQQC FQTTGAQSKYRLGNECETYAELKLGQELWKEGDK SFYLDTNVAYSVSQRDDWESTDPA FREANVQGKNLIESLPGSTIWAGKRFYQRHDVHM IDFYWWDISGPGAGLETIDLGFVK LSVAATRNSSESGSSAWIDNQRENKYTINNVD VRLAGLETNPGGSLELGVDYGRAD TQEGYSLAPNASKDGVMLTAEHTQSLMGGFNKVF VQYATDSMTSYNTGHSQGTSVNNN GHLLRVIDHGAINLAEKWDMMYVALYQDIDLNN NGNTWYSVGVPRPMYKWTPI MSTLL EAGYDNVKSQHTGERNGQYKLTLAQQWQAGDSIW SRPAIRVFATYANWDEKKGYSDDT GVAQDGTIGTNSRGKNNEVTFGAQFEAWW"
gene	47912..48841	/gene="malM"
CDS	47912..48841	/locus-tag="y0033" /gene="malM" /locus-tag="y0033" /function="phenotype; degradation of small molecules; Carbon compounds" /note="residues 7 to 309 of 309 are 51.80 pct identical to residues 3 to 306 of 306 from E. coli K12 : B4037; residues 7 to 309 of 309 are 50.98 pct identical to residues 3 to 305 of 305 from GenPept : >gb AAL23056.1 (AE008898) periplasmic protein of mal regulon [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="periplasmic protein of mal regulon"

		<pre> /protein-id="AAM83628.1" /db-xref="GI:21956692" /translation="MYEGITMKKNLLSLCLVLAL GGTAPLAVQAASTISPANVSIAPT ISTTTLQQLPWQPLVPPVTQDIQLTAGSPHISQG EVEGAVAAAFALPADRGSLVTLSS LLTDKQLFTPSVLVLDEQMRPAAYYPSSYFTYEK AGIMINDRLQGVMKLTPALGQKQI YLLVYTTRDDLKKTQLLDPAKAYAQGVGNAVPD IPDPIVNHSPGTGLRIKVTSEQGM GNIMIGLIQSAPTSAPVVVGSSIQPVAAPQSEPA KPAAPMLGETENYFNQAIKDAVKA GDVDKALKLLNEAEHLGSTSARKTFIGSVKGKG" </pre>
gene	complement(49078..49236)	/locus-tag="y0034"
CDS	complement(49078..49236)	/locus-tag="y0034"
		<pre> /note="residues 5 to 52 of 52 are 34.00 pct identical to residues 508 to 557 of 597 from GenPept : >gb AAF30492.1 AE002108-5 (AE002108) DNA polymerase III gamma-tau subunits [Ureaplasma urealyticum]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83629.1" /db-xref="GI:21956693" /translation="MTKKVAIIGVNLFI DVTHL CINKYCKSFSLCSQIPIERKPNL NVILNKKE" </pre>
gene	49240..49590	/locus-tag="y0035"
CDS	49240..49590	/locus-tag="y0035"
		<pre> /note="residues 37 to 95 of 116 are 39.39 pct identical to residues 12 to 74 of 476 from GenPept : >emb CAC05244.1 (AL391604) DNAJ domain protein similar to human tetratricopeptide repeat protein and protein kinase inhibitors [Schizosaccharomyces pombe]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83630.1" /db-xref="GI:21956694" /translation="MTLNMTGSSSLVVEKNPVGNF LKFAMNFPNL LLLFSDGTLIKQVE RELKTHLICNEFVKNKSKI VTVYITLGNDALLLI YYSNRVFYKKS YIKCGDIACMNYT VNEGyltTEIILWR" </pre>
gene	complement(49742..50260)	/locus-tag="y0036"
CDS	complement(49742..50260)	/locus-tag="y0036"
		<pre> /note="residues 1 to 172 of 172 are 80.23 pct identical to residues 1 to 172 of 172 from GenPept : >gb AAG54535.1 AE005199-5 (AE005199) Z0266 gene product </pre>

		[Escherichia coli O157:H7 EDL933]"
		/codon-start=1
		/transl-table=11
		/product="hemolysin co-regulated protein"
		/protein-id="AAM83631.1"
		/db-xref="GI:21956695"
		/translation="MPTPAYISITGKTQGNITAG AFTAESVGNIIYVQGHEDMLVQEF EHIVTVPTDPQSGQPSGQRAHKPLRFTVAYNKAV PLLYNALASGEMLPVELKWYRTS IEGKQEHFFTTKLEDATIIDIDCKMPHCQDSTKA EFTQLVRVSLAYRKINWDHTTAGT SGADDWRAPIEA"
gene	50781..51281	/locus-tag="y0037"
CDS	50781..51281	/locus-tag="y0037"
		/note="residues 2 to 166 of 166 are 62.65 pct identical to residues 1 to 166 of 166 from GenPept : >gb AAG54533.1 AE005199-3 (AE005199) Z0264 gene product [Escherichia coli O157:H7 EDL933]"
		/codon-start=1
		/transl-table=11
		/product="conserved hypothetical protein"
		/protein-id="AAM83632.1"
		/db-xref="GI:21956696"
		/translation="MMSKNKQSSVAPKERINIKY VPNTGDQVAEIELPLNLLVVGDLK GVREETSIEERQVSVNKNFNFSVMNEANISLSF NVPNRLEGDGEEDMPVALSIKGLD DFSPDNVAKKVPPELKKILELREALVALKGPLGNI PAFRSRLQDLLGNEDMREQLLKEI DILNQK"
gene	51349..52830	/locus-tag="y0038"
CDS	51349..52830	/locus-tag="y0038"
		/note="residues 20 to 492 of 493 are 76.95 pct identical to residues 19 to 491 of 492 from GenPept : >gb AAF96022.1 (AE004353) conserved hypothetical protein [Vibrio cholerae]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83633.1"
		/db-xref="GI:21956697"
		/translation="MPLHEENTVLAEPASATFL LDEIMSQTRMAPGNDGYDIAKQGV AAFISSILDTGTNEEPINKLLVDRMIIELDKKLS AQMDIEILHANEFREIESSWRSCLK LVDRTDFRENIKINIMHATKEELLEDFFESPEII QSGFYKHVYSSGYQFGGEPTAAI IGNYAFNNSSPDMKLLQYVSAVGAMAHAPFLSSV APDFFGISSFTLPAIKDLKSVFE GPAHTKWRALRESEDSRYLGLTTPRFLRLPYST VENPIKNFNYYEDVSRNHEHFLWG NTAFLLASCLTDSFAKYRWCPNIIGPQSGGTVHD LPVHLYEAMGQIQAKIPTEVLITD RREFELAEEGFITLTMRKGSDNAFFSANSVQKP KVFPNTREGKMAETNYKLGTQLPY

		MFVINRLAHYIKVLQREQIGSWKERQDLERELNI WLKQYIADQENPPTDVRSRRLRS AQIQVLDVEGDPGWYQVAMQVRPHFKYMGASFEL SLVGRLDKE"
gene	52837..53277	/locus-tag="y0039"
CDS	52837..53277	/locus-tag="y0039" /note="residues 11 to 140 of 146 are 35.87 pct identical to residues 8 to 134 of 137 from GenPept : >gb AAG54530.1 AE005198-11 (AE005198) Z0261 gene product [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83634.1" /db-xref="GI:21956698" /translation="MAALLNWDGSSASLFDRIQ GKGASSSDGRLRELLNSIQKHLN EVLNSRPGACQSAVDLGVIDLNDATATSSDFRKS IEKAIKDCIENYEPRISAVTVQSL LNHGDPLQLSFHISARVNFDDMGDVVEFNIQLDN NRRYCFNQET"
gene	53277..54503	/locus-tag="y0040"
CDS	53277..54503	/locus-tag="y0040" /note="residues 4 to 365 of 408 are 49.58 pct identical to residues 5 to 367 of 616 from GenPept : >gb AAG54529.1 AE005198-10 (AE005198) Z0260 gene product [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83635.1" /db-xref="GI:21956699" /translation="MSFEKYFRDEL DYLRQLGRD AAIERPHLAAFLSEQGSDPDVERL LEGFAFLTGNLREKIDDQFPELTHGLLNMLWPNY LRPIPSMTIIEYTPDES VVTEATL VKRGSQVMSIPIAQNGQSAFINSNAHAGPQCTF TLCRDVWLFPM SIREISANSSNEQ GILSIHFAAKAELNLQDLQLDKLRFYLGEDNYTS TQLYFWINHYFERAELVNGITIP MPDFDFNPVGFERDDALLPYPKNAYMGYRILQEY FCFPEGFLFFDVNGVVD FPPHLNA SEFSLNLYFSQALPPEVKVRSTTLRMNCTPAVNL FQHDSEAIDL DGTQTEYPLCVSYH NPDHYDIFSVD RVD SWLSEKGV PKGRGRALNPKT WTSALLLFYLSPVFCRTHSACFQA NALCIVIMDIFYNVTL"
repeat-region	complement(54361..54622)	/note="insertion element; partial"
)	/insertion-seq="IS1661"
gene	complement(54393..54650)	/locus-tag="y0041"
)	
CDS	complement(54393..54650)	/locus-tag="y0041"
)	/function="IS and transposon related functions"

```

        /note="IS1661 orfB; residues 5 to  

        84 of 85 are 60.49 pct identical  

        to residues 158 to 238 of 240 from  

        GenPept : >emb|CAA63547.1|  

        (X92970) orfB [Escherichia coli]"  

        /codon-start=1  

        /transl-table=11  

        /product="putative transposase"  

        /protein-id="AAM83636.1"  

        /db-xref="GI:21956700"  

        /translation="MDHFSSVVDRIQSMSRKGN  

        CLDNAVMENFFSHLKAEMYHRKKY  

        DSATVLKRDIVEYIHYNTERISLKTGGMSPAEY  

        RTQVEKQ"  

repeat-region    complement(54623..56576 /note="insertion element"  

                )  

                /insertion-seq="IS100"  

gene            complement(54689..55471 /locus-tag="y0042"  

                )  

CDS             complement(54689..55471 /locus-tag="y0042"  

                )  

                /function="IS and transposon  

                related functions"  

                /note="IS100; orfB; residues 1 to  

                260 of 260 are 100.00 pct  

                identical to residues 1 to 260 of  

                260 from GenPept : >gb|AAC69770.1|  

                (AF074612) putative transposase  

                [Yersinia pestis]"  

                /codon-start=1  

                /transl-table=11  

                /product="putative transposase"  

                /protein-id="AAM83637.1"  

                /db-xref="GI:21956701"  

                /translation="MMELQHQRMLALAGQLQLE  

                SLISAAPALSQQAVDQEWSYMDFL  

                EHLLHEEKLARHQKQAMYTRMAAFPVKTFEEY  

                DFTFATGAPQKQLQSLRSLSFIER  

                NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF  

                TTAADLLLQLSTAQRQGRYKTTLQ  

                RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIAGR  

                YEKSAMILTSNLFPFGWDQTFFAGD  

                AALTSAMLDRILHHSHVQIKGESYRLRQKRKAG  

                VIAEANPE"  

gene            complement(55468..56490 /locus-tag="y0043"  

                )  

CDS             complement(55468..56490 /locus-tag="y0043"  

                )  

                /function="IS and transposon  

                related functions"  

                /note="IS100; orfA; residues 1 to  

                340 of 340 are 100.00 pct  

                identical to residues 1 to 340 of  

                340 from GenPept : >gb|AAC13168.1|  

                (AF053947) putative transposase  

                [Yersinia pestis]"  

                /codon-start=1  

                /transl-table=11  

                /product="putative transposase"  

                /protein-id="AAM83638.1"  

                /db-xref="GI:21956702"  

                /translation="MVTFETVMEIKILHKOGMS

```


		RAIARELGISRNTVKRYLQAKSEP PKYTTPRPAVASLLDEYRDYIRQRIADAHYPKIPA TVIAREIRDQGYRGMTILRAFIR SLSVPQEQEPAVRFETEPGRQMQVDWGTMRNGRS PLHVFVAVLGYSRMLYIEFTDNMR YDTLETCHRNAFRFFGGVPREVLYDNMKTIVVLQR DAYQTGQHRFHPSLWQFGKEMGFS PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRL RPMGITVDVETANRHGLRWLHDVA NQRKHETIQARPCDRWLEEQQSMLALPPEKKEYD VHLDENLVNFDKHPLHHPLSIYDS FCRGVA"
gene	56560..56985	/locus-tag="y0044"
CDS	56560..56985	/locus-tag="y0044" /function="IS and transposon related functions" /note="IS1541a; residues 6 to 141 of 141 are 100.00 pct identical to residues 17 to 152 of 152 from GenPept : >gb AAL27370.1 AF426171-1 (AF426171) transposase [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83639.1" /db-xref="GI:21956703" /translation="MHRSLHIVFAPKYRRQVFYR EKRRRAIGSILRKLCWKNVNILEA EYCVDHIHMLLEIPKMSVSGFMGYLKGKSSMLL YEQFGDLKFKYRNREFWCRGYIVD TVGKNTARIQEYIKHQLEEDKMGEQLSIPYPGSP FTGRK"
repeat-region	56575..57091	/note="insertion element; partial" /insertion-seq="IS1541a"
gene	complement(57193..57432)	/locus-tag="y0045"
CDS	complement(57193..57432)	/locus-tag="y0045" /note="residues 1 to 79 of 79 are 75.94 pct identical to residues 3 to 81 of 81 from E. coli K12 : B3928; residues 1 to 79 of 79 are 77.21 pct identical to residues 1 to 79 of 79 from GenPept : >gb AAL22928.1 (AE008891) putative cytoplasmic protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83640.1" /db-xref="GI:21956704" /translation="MSFEVFEKLEVKVQQAIDTI TLLQMEIEELKEKNNTLTQEVQDA AGSREALVRENEQLKQEQHVWQDRLRALLGKMEE V"
gene	58060..58908	/gene="glpF" /locus-tag="y0046"
CDS	58060..58908	/gene="glpF" /locus-tag="y0046" /function="transport; transport of

gene 59085..60608
CDS 59085..60608

small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 1 to 282 of 282
are 82.62 pct identical to
residues 1 to 279 of 281 from E.
coli K12 : B3927; residues 1 to
282 of 282 are 82.62 pct identical
to residues 1 to 279 of 281 from
GenPept :
>gb|AAG59120.1|AE005623-11
(AE005623) facilitated diffusion
of glycerol [Escherichia coli
O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="facilitator for glycerol
uptake"
/protein-id="AAM83641.1"
/db-xref="GI:21956706"
/translation="MSQTASSTLKGQCIAEFLGT
GLLIFFGAGCVAALKLAGASFGQW
EISIIWGLGVAMAIYLTAAISGAHLNPAVTIALW
LFACFERRKVLPIYIVAVAGAFCA
AALVYGLYYSLFVDFEQTHQMVRGSTESLQLAGI
FSTYPNPHISVVQAFLVETVITAI
LMCLILALTDGNGIPRGPLAPLLIGILIAVIGA
SMGPLTGFA LNPARDLGPKAFSYL
AGWGDI AFTGGRDIPYFLVPIFGPIVGALLGAFG
YRALIGRHLPCDVCTLEDEESTTI TTERKA"
/gene="glpK"
/locus-tag="y0047"
/gene="glpK"
/locus-tag="y0047"
/function="enzyme; central
intermediary metabolism: Pool,
multipurpose conversions"
/note="residues 7 to 507 of 507
are 84.63 pct identical to
residues 2 to 502 of 502 from E.
coli K12 : B3926; residues 5 to
507 of 507 are 84.49 pct identical
to residues 7 to 509 of 509 from
GenPept :
>gb|AAG59119.1|AE005623-10
(AE005623) glycerol kinase
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="glycerol kinase"
/protein-id="AAM83642.1"
/db-xref="GI:21956707"
/translation="MTTENTTQKKYIVALDQGTT
SSRAVVL DHNANIVSVSQREFTQI
YPKAGWEHDPMEIWATQSSTLIEVLAKAGINS
EIAIGITNQRETTIVWDKVTGKP
VYNAIVWQCRRTADICEKLKKEGLEEYIRHNTGL
VVDPYFSGTKVKWILDNVEGARER
AERGELLFGTVDTWLVWNMTQGRVHVTDYTNASR
TMMFNIRTKEWDDRMLKALNIPRA
MLPEVRPSSEIYGKTNIGGKGGTRIP IAGIAGDQ
QAALFGQLCVQPGMAKN TYGTGCF
LLMNTGEEAVQSTHGLLTTIACGPRGEVNYALEG

		AVFIGGASIQWLRDELKLIGDATD SEYFATKVKNSNGVYVPAFTGLGAPYWDPYARG AIFGLTRGVNSNHIIRATLESIA QTRDVLDAQADSGARLKSLRVDGGAVANNFLMQ FQADILGTRVERPAIRESTALGAA FLAGLATGFWDLLDEVKSKASIEREFRPGIETTE RDIRYKGWKKAVARARDWEEHDE"
gene	60737..61855	/gene="glpX" /locus-tag="y0048"
CDS	60737..61855	/gene="glpX" /locus-tag="y0048" /function="phenotype; Not classified" /note="unknown function in glycerol metabolism; residues 37 to 372 of 372 are 84.22 pct identical to residues 1 to 336 of 336 from E. coli K12 : B3925; residues 37 to 372 of 372 are 84.22 pct identical to residues 1 to 336 of 336 from GenPept : >dbj BAA09535.1 (D55718) GlpX [Klebsiella aerogenes]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83643.1" /db-xref="GI:21956708" /translation="MRVKRVQLTPLRLQVRKVIE FLPIFSFSIPQSTGLTMKRELAIE FSRVTEAAALAGYKWLGRGDKNAADGA AVQAMRI MLNQVNIDGRIVIGEGEIDEAPML FIGEHVGTGQDAVDIAVDPIEGTRMTAMQANA LAVLAVGDQGTFLHAPD MYMEKLV VGPAAKGAIDLNLPLEQNLCNIATALNKPLADLT VITLAKPRHDGIIAAMQQLGVKVF AIPDGDVAASILTCMPESEVDVMYCIGGAPEGVI SAAVIRALDGD MQGRLLPRHQVKG DSEDNRRIGE QELLRCKSMGIEAGNVLQLGDMAR NDNVIFSATGITKGD LLEGIYRKG NMATTETLLIRGKSRTIRRI RSTHFLDRKDPALH EFL"
gene	62010..62756	/gene="fpr" /locus-tag="y0049"
CDS	62010..62756	/gene="fpr" /locus-tag="y0049" /function="enzyme; central intermediary metabolism: Pool, multipurpose conversions" /note="residues 1 to 248 of 248 are 74.19 pct identical to residues 1 to 248 of 248 from E. coli K12 : B3924; residues 1 to 248 of 248 are 77.01 pct identical to residues 1 to 248 of 248 from GenPept : >gb AAL22924.1 (AE008890) ferredoxin-NADP reductase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="ferredoxin-NADP"

		reductase" /protein-id="AAM83644.1" /db-xref="GI:21956709" /translation="MAEWVSGKITHIEHWTDALF SLQVNAPVDPFTAGQFAKLALDIN GERVQRAYSIVNAPSDHNLEFYLVTVPEGKLSPR LDQLSVGGEVMITKQAAGFFVLEE IPDCDTLWMLATGTAIGPYLSILQEGQDLERFKH LVLVHAARFAHDLSYLPLMQQLEQ RYNGKLRIQTVVSREESPGSLTGRVPALIENGAL EAAVGLKIDAKDSHVMLCGNPQMV RDTQQLLKEQREMRKHLRRKPGHMTSEQYW"
gene	complement(63097..63597	/locus-tag="y0050"
)	
CDS	complement(63097..63597	/locus-tag="y0050"
)	
		/note="residues 23 to 163 of 166 are 66.66 pct identical to residues 1 to 141 of 146 from E. coli K12 : B3921" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83645.1" /db-xref="GI:21956710" /translation="MVSCDLEVHFAEIMLGKWIC SSMTIQQWCFSFKGRIGRREFWIW MGLWLLAMLVIFTLAGKEWLPIQSASFALVFLW PTAAVVVKRLHDRNKAGWWALLAV LAWMLMAGNWQMLTPIWQWGVGRFIPTLIFVMMF IDCGAFLGTEGDNRFGEAVPVKF FADKAK"
gene	63700..64314	/locus-tag="y0051"
CDS	63700..64314	/locus-tag="y0051"
		/note="residues 11 to 204 of 204 are 56.18 pct identical to residues 10 to 193 of 199 from E. coli K12 : B3920; residues 10 to 203 of 204 are 57.21 pct identical to residues 7 to 192 of 198 from GenPept : >gb AAL22922.1 (AE008890) putative periplasmic protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83646.1" /db-xref="GI:21956711" /translation="MRIILLLAALLLITFMLITT INHAHADPTNDSSPPKEGAPPIAP YLLFNAPTFDLTLVKFRESYNRANPTLPINEFHA ITVKEDSPPLTRAASKINENLYAS TALEKGTGKIKTLQITYLPIKGNEEKTAALLAIN YMAALMRQFEPTLSVVQSLANVQK LLTEGKGSPFYAHTIGAIRYVVADNGEKGLTFAV EPIKLSLSEA"
gene	64443..65210	/gene="tpiA"
		/locus-tag="y0052"
CDS	64443..65210	/gene="tpiA"
		/locus-tag="y0052"
		/function="enzyme; energy metabolism, carbon: Glycolysis"

```

/feature "note" {
    /note="residues 1 to 255 of 255
are 82.35 pct identical to
residues 1 to 255 of 255 from E.
coli K12 : B3919; residues 1 to
255 of 255 are 84.70 pct identical
to residues 1 to 255 of 255 from
GenPept : >gb|AAD16183.1|
(AF098509) triose phosphate
isomerase [Enterobacter cloacae]"
/codon-start=1
/transl-table=11
/product="triosephosphate
isomerase"
/protein-id="AAM83647.1"
/db-xref="GI:21956712"
/translation="MRHPLVMGNWKLNGSTHMVN
ELIAGLRKELSTVDGCGVAIAPPA
IYLNQAKHELAGSRIALGAQNVVDNLSGAFTGET
SAEMLKDIGAQYIIIIGHSEERRYH
QESDELIAKKFGVLKEIGLIPVLCIGESEAEAEA
GQTEAVCAKQLDAVLNLTGVKAFE
GAVIAYEPIWAIGTGKSATPAQAQAVHKFIRDHI
AKQDAAVAAQVVIQYGGSVNDKNA
AELFTQPDIDGALVGGASLKADAFVIVKAAKA
KKA"
}

gene complement(65442..66737 /locus-tag="y0053"
)
CDS complement(65442..66737 /locus-tag="y0053"
)

/feature "function" {
    /function="regulator"
    /note="residues 28 to 405 of 431
are 30.26 pct identical to
residues 4 to 358 of 383 from
GenPept : >emb|CAB87565.1|
(AJ277295) FldY protein
[Sphingomonas sp. LB126]"
/codon-start=1
/transl-table=11
/product="putative transcriptional
regulator"
/protein-id="AAM83648.1"
/db-xref="GI:21956713"
/translation="MPKRQVLFKLKKLNKITRRN
MQKKNDNRNSIKIMQIRAFCMTAEQ
GAASLAALNLFRTQSAITRSIRDLEHTLAISLFE
RHAKGMLLTDLGNVILPRARSAME
ELTRIPALLRRLQQRDDEGIEDLEPTWLFNERRL
QIFLSLYRQQHALHVAQALDITQS
AVSAALKVLEKGAGMYLFHRTPKGMLPTPAGHEI
APCISRALNALHHIPEEITAHRGD
LTGSRVVGALPLSRARLLPQAMIKLISRHPGIKI
VTNESGFTALIAELRAGDIDFIIG
ALRNEKMLLDIHSEILFEEELILLARPNNHPLSDR
RVKNQELKDIQWVLPNRNHAPSRHL
LEVAFCKMGLASPQPVVESGDPVAVRALLGSDM
VAAVSSHQQLDFEVSEGILIPQVN
LTGTRREIGLMTRQKALNSPATDALINCVREVIQ
SSNDK"
}

gene 66730..67551 /locus-tag="y0054"
CDS 66730..67551 /locus-tag="y0054"
/feature "note" {
    /note="residues 34 to 272 of 273
are 65.41 pct identical to

```

		residues 3 to 238 of 244 from GenPept : >emb CAC46343.1 (AL591788) conserved hypothetical protein [Sinorhizobium meliloti]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83649.1" /db-xref="GI:21956714" /translation="MGNKTHYFPLIKPCQNPRQL KQQKKEKDMAMIPQKTALVVSAS ADFVWRAGGAIALHVEQGYQVHIVCLSYGERGES AKLWRKGDMEERVKASRHTEAQA AANVLGASIEFFDMGDYPLRADKESLFRADVFR RIQPHFVLTHSLADPYNIDHPLAA NLAQEARIIAQAEGYRPGAEIIGAPPVYCFEPHQ PEQCGWKPDVLLDITSVWEKKYAA IQCMAGQEHLWEYYTRVALQRGVQAKRNIGIAST KTIIHGEGYQSLFPRVTEDLS"
gene	67548..68261	/locus-tag="y0055"
CDS	67548..68261	/locus-tag="y0055" /note="residues 6 to 229 of 237 are 61.60 pct identical to residues 1 to 224 of 224 from GenPept : >emb CAB87566.1 (AJ277295) FldZ protein [Sphingomonas sp. LB126]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83650.1" /db-xref="GI:21956715" /translation="MSLVNMKGVVVTNIERAELA LLQRFAYEGVATVHEAQLRQGLLD ERIKPIQQGRCIAGNAVTVLVTPGDNWMFHVAVE QCQPGDVLLVAPTSECHDGFFGDL LATSLARGVVALVGDIGIRDSQTLREMNFPVWS RAVWAQGTVKASLGSVNVPVICAG QLVNPBGDIVVADDDGVVIVPREQATAIADAAQTR VDLETSKRQRLANGELGLDIYQMR APLAKKGLRYVNSLNALKS"
gene	68327..69754	/locus-tag="y0056"
CDS	68327..69754	/locus-tag="y0056" /note="residues 2 to 471 of 475 are 52.20 pct identical to residues 3 to 471 of 477 from E. coli K12 : B0770; residues 2 to 471 of 475 are 52.20 pct identical to residues 3 to 471 of 477 from GenPept : >gb AAG55099.1 AE005254-11 (AE005254) putative membrane pump protein [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative membrane pump protein" /protein-id="AAM83651.1" /db-xref="GI:21956716" /translation="MKNKIWKLCILVMIPLVIWF IPPPEGLTELSWRLSGFYLAICG"

		LILKPFSEAVVLLGVVGFAGFFLNNTSQILVGYA TSTVWLVFAAFGISISFVKTLGR RIAFHMIRFCGSTTLRLGYVTAFLEFVISPVTPS NTARSGGIVFPIILSVVKALGSEP GDTAKKAGSYLMSNIYFVMKVSSFMTITAMAPNL LAADFAAKILGIHLDWGVWALAMV VPGLLLLLIVPAVGYYLDKPELKKVDNKKIADEG LAELGPITRNEKLLVGIFISALLG WALPSLLGQLFGITLKIDATAVAIMAMALCILLG VIKWDDVLQNKGAWNTLLWFGGII GLASALSKEKVFDWLANLIQNNVDFGHNPFIALT IIGFLSIIIRYFFASASSYAIAML PVFLTGVKVAGADPMALALVLAATNSYGGALTHY GGGSAPIIFGAGYNNVKQWWASGA VIATVCFIVTMTVGYVWWQFLGFVK"
gene	69830..70648	/gene="modA"
		/locus-tag="y0057"
CDS	69830..70648	/gene="modA" /locus-tag="y0057" /function="putative transport; transport of small molecules; Other" /note="residues 48 to 271 of 272 are 55.55 pct identical to residues 5 to 229 of 230 from GenPept : >dbj BAB21454.2 (AB050935) ProX protein [Pseudomonas straminea]" /codon-start=1 /transl-table=11 /product="molybdate-binding periplasmic protein precursor" /protein-id="AAM83652.1" /db-xref="GI:21956718" /translation="MACLLAQYNSGDILMKYSNV IVSGLCMSMVSLATAAPTEVPSDE PVTLRIISSMATRQFLTEVIAQFAQQSKYQVELE SVGGVDATKRVEAGEAFDVVILSA NAIDKLIDSGKILPNSRIDLVKSGVAIAVKEGAQ IMDVSSEETVKQAVLAANTIAYST GPSGVYLTEVFHGWGIAEQIKDRIVKVPVGPVPG SLVAKGEVELGFLQLSELLHLKGI IILGPLPTDIQIMTHFSAGVPLKTNQKAIKVLL DFLASPAATEAKIKNGMEPI"
gene	complement(70898..71920)	/gene="sbp"
		/locus-tag="y0058"
CDS	complement(70898..71920)	/gene="sbp" /locus-tag="y0058" /function="transport; transport of small molecules; anions" /note="residues 12 to 340 of 340 are 83.58 pct identical to residues 1 to 329 of 329 from E. coli K12 : B3917" /codon-start=1 /transl-table=11 /product="periplasmic sulfate-binding protein of sulfate/thiosulfate ABC transporter"

```

/protein-id="AAM83653.1"
/db-xref="GI:21956719"
/translation="MITIIFLRSGSMRKWGVGLS
LLVLASGAMAKDIQLLNVSYPTR
EFYQEYNQAFSKYWQQQTGDKVTVRQSHGGSGKQ
ATSVINGIEADVVTLLALAYDVDAI
AERGRIDKNWIKRLPDNSAPYTSTIVFLVRKGNP
KQIHDWSDLVKPGTSVITPNPKTS
GGARWNYLAAWGYALEHNNNDQAKAQEFVNALYK
NVEVLDSGARGATNTFVERGIGDV
LIAWENEALLAVNEVGNGQFDIVTPSVSILAEP
VSVVDKVVDKRGTRDVADAYLKYL
YSPEGQTIAAKNYRPRDPVVAAKFAKEFPQLKL
FTIDEVFGGWTQAQKTHFATGGVF DEISKR"
gene      complement(72108..73091 /gene="pfkA"
)
CDS       /locus-tag="y0059"
complement(72108..73091 /gene="pfkA"
)
/locus-tag="y0059"
/function="enzyme; energy
metabolism, carbon: Glycolysis"
/note="residues 1 to 327 of 327
are 77.06 pct identical to
residues 1 to 320 of 320 from E.
coli K12 : B3916; residues 1 to
327 of 327 are 79.20 pct identical
to residues 1 to 320 of 320 from
GenPept : >gb|AAD16179.1|
(AF098509) phosphofructokinase
[Enterobacter cloacae]"
/codon-start=1
/transl-table=11
/product="6-phosphofructokinase I"
/protein-id="AAM83654.1"
/db-xref="GI:21956720"
/translation="MVKKIGVLTSGGDAPGMNAA
IRGVVRAALSAGLDVFGIEDGYLG
LYENRMKKLD RYVSVD MINRGGTF LG SARFPEFR
DPEVRKVALKNMHERGIDGLVVIG
GDGSYAGADLLTKEGGIHCVGLPGTIDNDVAGTD
YTIGFFTALETVVEAIDRLRDTSS
SHQRISIVEVMGRYCGDLTAAAIAGGCEFIAIP
EVEFKRDDLVAEIKAGIAKGKKHA
IVAITEKLDDIDSLAKYIEKETGRETRGTVLGH
IRGGAPVAYDRILASRMGAYAVDL
LLQDHDYKKGGFCVGVQNEKMHVHELISVCIAPEN
KKSFKEDWYDTAKKLF"
gene      complement(73309..74211 /locus-tag="y0060"
)
CDS       /locus-tag="y0060"
complement(73309..74211
)
/function="putative transport"
/note="residues 1 to 293 of 300
are 78.49 pct identical to
residues 1 to 293 of 300 from E.
coli K12 : B3915; residues 1 to
293 of 300 are 79.86 pct identical
to residues 1 to 293 of 300 from
GenPept : >gb|AAL22901.1|
(AE008889) putative CDF family
transport protein [Salmonella

```


		typhimurium LT2]"
		/codon-start=1
		/transl-table=11
		/product="putative efflux permease protein"
		/protein-id="AAM83655.1"
		/db-xref="GI:21956721"
		/translation="MDPQYARWVKAAALSATALA SILLIIKIFAWWHTGSVSLAALV DSLVDLAASLTNLFVVRYSLQPADEEHTFGHGKA ESLAALAQSMFISGSALFLFLTGF RHLASPEPLQDPSIGIGVTLVALFSTLILVTFQR WVVRKTHSQAIRADMLHYQSDVLM NGAILIALALSWYGFRRADALFALGIGVYILYSA LRMGYEAVQSLLDRALPDDERQQI IDIVTSWPGVIGAHDLRTRRSQGTRFIQLHLEME DMMPLMEAHVLAEQVEHALLYRFP GADVLIHQDPCSVVPKERHAHWEL"
gene	74583..74705	/locus-tag="y0061"
CDS	74583..74705	/locus-tag="y0061"
		/function="IS and transposon related functions"
		/note="unidentified IS; residues 2 to 37 of 40 are 47.22 pct identical to residues 89 to 124 of 253 from GenPept : >emb CAC35348.1 (AJ277063) putative transposase [Vibrio salmonicida]"
		/codon-start=1
		/transl-table=11
		/product="putative transposase"
		/protein-id="AAM83656.1"
		/db-xref="GI:21956722"
		/translation="MIFIDDNIIRTHQHGTGAVS ESDESIKKHRGVTRQKLISR"
gene	complement(74773..75732)	/locus-tag="y0062"
)	
CDS	complement(74773..75732)	/locus-tag="y0062"
)	
		/note="residues 15 to 314 of 319 are 56.00 pct identical to residues 4 to 287 of 292 from E. coli K12 : B3411; residues 16 to 319 of 319 are 62.01 pct identical to residues 6 to 313 of 313 from GenPept : >gb AAL23539.1 (AE006471) putative cytoplasmic protein [Salmonella typhimurium LT2]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83657.1"
		/db-xref="GI:21956723"
		/translation="MIAQEDAHDYHRPMKTTPTP HDALFKNFMFTQPATACDLLEFHLP PELRQLCDLSTLRLESGSFIENNLACYSVDVLYS LKTTVGDDGYVYALIEHQSSPDKHM AFRLMRYAIAAMQSHLEAGYDKLPLVIPILFYHG MVTYPYPMSWLHAFNQPELAGQL YCGNFPLVDVTVIPDHEIMTHRRIALLELLQKHI"

```

RQRDLSELDDQLVILIASGYTTED
QLKSAINYIIQVGETAPEVVFIRSLAHLRPEHEE
SLMTIAQKLEQKGEARGIVKGRVE
GRVEGAQETALKIARTMLANGLDRATVMKMTGLS
EEELTQIIHH"
gene      complement(75777..75953 /locus-tag="y0063"
)
CDS       complement(75777..75953 /locus-tag="y0063"
)
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83658.1"
/db-xref="GI:21956724"
/translation="MPSLLASTLQISPLYECINV
LTDVAVTINNQETDIQQLVACKHYR
VALMRTHAAPKSPQ"
gene      75932..76039 /locus-tag="y0064"
CDS       75932..76039 /locus-tag="y0064"
/note="residues 1 to 33 of 35 are
51.51 pct identical to residues
230 to 262 of 326 from GenPept :
>emb|CAB54522.1| (AJ245959) Int
protein [Bacteriophage WPhi]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83659.1"
/db-xref="GI:21956725"
/translation="MKQEVKANASGKLFNMDYGK
FGETQRNVKPDLPHG"
gene      76049..76252 /locus-tag="y0065"
CDS       76049..76252 /locus-tag="y0065"
/note="residues 1 to 56 of 67 are
80.35 pct identical to residues
269 to 324 of 326 from GenPept :
>emb|CAB54522.1| (AJ245959) Int
protein [Bacteriophage WPhi]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83660.1"
/db-xref="GI:21956726"
/translation="MLRHTCASHFMMNSRNIIAL
QQILRHANIQPTMAYAHLAPDYLQ
NTVILTPLKGGLAAETRPQSVHT"
gene      complement(76410..76898 /locus-tag="y0066"
)
CDS       complement(76410..76898 /locus-tag="y0066"
)
/note="residues 51 to 162 of 162
are 62.50 pct identical to
residues 1 to 112 of 122 from E.
coli K12 : B3914; residues 1 to
162 of 162 are 52.46 pct identical
to residues 1 to 156 of 166 from
GenPept : >gb|AAL22900.1|
(AE008889) periplasmic repressor
of cpx regulon by interaction with
CpxA, rescue from transitory
stresses [Salmonella typhimurium
LT2]"

```

		/codon-start=1 /transl-table=11 /product="putative solute-binding periplasmic protein of ABC transpoter" /protein-id="AAM83661.1" /db-xref="GI:21956727" /translation="MRKVTTLVMA SMFVLGSSAA FAADNTKVTEGYHGDGKMMMNKKG DRGHHNMF DGINLTEQQRQQMRDLMRQSHQSQPR LDLEDREAMHKLITADKFDEAAVR AQA EKMSQNQIERHVEMAKVRNQMYNLLTPEQKE ALNKKHQERIEKLQQKPAAPSSA QK"
gene	77048..77770	/gene="cpxR"
CDS	77048..77770	/locus-tag="y0067" /gene="cpxR" /locus-tag="y0067" /function="putative regulator" /note="residues 9 to 238 of 240 are 90.43 pct identical to residues 1 to 230 of 232 from E. coli K12 : B3912" /codon-start=1 /transl-table=11 /product="transcriptional regulator in 2-component system" /protein-id="AAM83662.1" /db-xref="GI:21956728" /translation="MRQRGEITMHKILLVDDRE LTSLLKELLEMEGFNVVAYDGEQ ALSQLDSSIDL LLLDIMMPRKNGIETLKE LRQH QTPVIMLTARGSELDRVLGLELGA DDYLAKPFNDRELVARIRAILRRSNWSEQQNAE QGAPTLEVDCLQLNPGRQEASFEG QPLELTGTEFTLLYLLAQHLGQVVSREHLSQEVL GKRLTPFDRAIDMHISNLRRLPD RKDGLPWFKTLRGRGYLMVSET"
gene	77767..79143	/gene="cpxA"
CDS	77767..79143	/locus-tag="y0069" /gene="cpxA" /locus-tag="y0069" /function="putative regulator; global regulatory functions" /note="acting on arcA; residues 1 to 454 of 458 are 80.83 pct identical to residues 1 to 454 of 457 from E. coli K12 : B3911" /codon-start=1 /transl-table=11 /product="probable sensor protein, histidine protein kinase" /protein-id="AAM83663.1" /db-xref="GI:21956729" /translation="MINSLTTRIFAIFWFTLALV LMLVLMVPKLD SRQLTVLLDSEQR QGTMLEQHIEAELANDPANDLMWWRRLHRAIEKW APPGQHLILVTSEGRIIGVQRQEV QMVRNFIGQSDNADQPKKKKYGRVEMVGPFSIRD GEDNYQLYLIRPANSPQSDFINLM FDRPLLLLIATMLISAPLLLWLAWSLAKPARKLK NAADDVARGNLKQHPELESGPQEF LATGASFNQMISSLDRMVVAQQRLISDISHELRT

```

PLTRLQLATALMRRRHGEGKELER
IEMEAQRLDSMINDLLVLSRSQHKNELHREPIKA
DELWSDVLENAQFEAEQMGKTLVV
TAPPGPWPLFCNPAALDSALENIVRNALRYSHHH
IAVAFSIDNQGVTTIIVDDDGPVVS
PEDREQIFRPFYRTDEARDRASGGTGLGLAIVET
AVSQHRGWVKAEDSPLGGLRLIVW LPLHPLKS"
gene      complement(78938..79090 /locus-tag="y0068"
)
CDS       complement(78938..79090 /locus-tag="y0068"
)
          /codon-start=1
          /transl-table=11
          /product="hypothetical"
          /protein-id="AAM83664.1"
          /db-xref="GI:21956730"
          /translation="MGYLRLLPDADSPRFQQL
PGPILFLPTPDLGLHLYDKMAGIF VHGPLG"
gene      complement(79192..80256 /gene="ada"
)
          /locus-tag="y0070"
CDS       complement(79192..80256 /gene="ada"
)
          /locus-tag="y0070"
          /function="enzyme; DNA -
          replication, repair,
          restriction/modification"
          /note="residues 6 to 350 of 354
          are 52.75 pct identical to
          residues 10 to 353 of 354 from E.
          coli K12 : B2213; residues 6 to
          345 of 354 are 65.58 pct identical
          to residues 18 to 357 of 360 from
          GenPept : >emb|CAD16277.1|
          (AL646070) probable ADA regulatory
          of adaptative response contains:
          methylated-DNA--protein-cysteine
          methyltransferase EC 2.1.1.63
          O-6-methylguanine-DNA
          transcription regulator[Ralstonia
          solanacearum]"
          /codon-start=1
          /transl-table=11
          /product="O6-methylguanine-DNA
          methyltransferase; transcription
          activator/repressor"
          /protein-id="AAM83665.1"
          /db-xref="GI:21956731"
          /translation="MNNVKDPRWAAIINRDKTAD
          GQFVYAVKTTGIYCRPSCPSRAK
          AENIEFFIDNTAAEQAGYRCKRCQPTQLSRAQQ
          QVEKISQACRLIELAETPPKLNEL
          AAQLGLSTFYFHRLFKAITGLTPKGYANATRSE
          IRAQLSHGGSVTD AIFEAGYNSSS
          RFYAQSQQLGMPTRYRKGGCDARLHFAVGESS
          LGAILVAKSELGVCAILLGDDPVR
          LVQQLQDKFPQANLVGGDAEFEQWVAQVVGCV
          EAPKLGLNLPLDIRGTAFQQRVWQAL
          REIPIGETASYADIASRIGSPTAVRAVAGACAA
          N ILAVAIPCHR VIRQDGALSGYRWG
          VERKRLLLEREGVEKEAEDH"
gene      80349..80933 /locus-tag="y0071"

```

CDS	80349..80933	/locus-tag="y0071" /note="residues 33 to 194 of 194 are 80.24 pct identical to residues 1 to 157 of 157 from E. coli K12 : B3606" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83666.1" /db-xref="GI:21956733" /translation="MLLNFCFTPPLLATAALNKG FWYPAPLIIGGHMLNIVLFEPEIP PNTGNIIRLCANTGCQLHLIKPLGFTWDDKRLRR AGLDYHEFADIKHHHDYQAFLDSE KLDSTQPARLFALTTKGTPAHSVSYQANDYLLF GPETRGLPAYILDALPAQQKIRIP MQADSRSMNLSNAVSVVVYEAWRQLGYPGALLKE "
gene	complement(81056..81880)	/gene="cysE"
CDS	complement(81056..81880)	/locus-tag="y0072" /gene="cysE" /locus-tag="y0072" /function="enzyme; amino acid biosynthesis: Cysteine" /note="residues 2 to 274 of 274 are 86.08 pct identical to residues 1 to 273 of 273 from E. coli K12 : B3607" /codon-start=1 /transl-table=11 /product="serine acetyltransferase" /protein-id="AAM83667.1" /db-xref="GI:21956734" /translation="MMSSEELEQVWSNIKSEARA LAECEPMLASFFHATLLKHENLGS ALSYILANKLANPIMPAIAIREVVVEEAYRSDAHM IVSAARDILAVRLRDPVVDKYSTP LLYLKGFFHALQAYRIGHWLWAQDRKALAIYLNQ VSVAFGVDIHPAATIGCGIMLDHA TGIVIGETAVVENDVSILQSVTLGGTGKTSGDRH PKIREGVMIGAGAKILGNIEVGRG AKIGAGSVVLQSVPAHTTAAGVPARIVGKPESDK PSLDMDQHFNGSIQGFYGDGI"
gene	complement(82143..83162)	/gene="gpsA"
CDS	complement(82143..83162)	/locus-tag="y0073" /gene="gpsA" /locus-tag="y0073" /function="enzyme; energy metabolism, carbon: Aerobic respiration" /note="residues 1 to 336 of 339 are 84.52 pct identical to residues 1 to 336 of 339 from E. coli K12 : B3608" /codon-start=1 /transl-table=11 /product="glycerol-3-phosphate

```

dehydrogenase (NAD+) "
/protein-id="AAM83668.1"
/db-xref="GI:21956735"
/translation="MNTNPASMAVIGAGSYGTAL
AITLARNGHQVVLWGHDPKHIQQL
QQDRCNRAFLPDAAFPDTRLRLETDLACALAASRD
VLVVVPSHVFGAVLHQLKPHLRKD
ARIVWATKGLEAETGRLLQDVAREVLGEAIP LAV
ISGPTFAKELAAGLPTAIALASTD
VQFSEDLQQLLHCGKSFRVYSNPDFIGVQLGGAV
KNVIAIGAGMSDGIGFGANARTAL
ITRGLAEMTRLGTALGADPSTFMGMAGLGDLVLT
CTDNQSRNRRFGIMLGQGLGVKEA
QDNIGQVVEGYRNTKEVLALAQRHGVEMPITEQI
YQVLYCHKNAREAAALTLLGRTKKD EKIGI"
gene      complement(83162..83638 /gene="secB"
)
CDS      complement(83162..83638 /gene="secB"
)
        /locus-tag="y0074"
        /function="transport; protein,
        peptide secretion"
        /note="may bind to signal
        sequence; residues 1 to 158 of 158
        are 91.13 pct identical to
        residues 1 to 155 of 155 from E.
        coli K12 : B3609"
        /codon-start=1
        /transl-table=11
        /product="protein export;
        molecular chaperone"
        /protein-id="AAM83669.1"
        /db-xref="GI:21956736"
        /translation="MSEQNNTEMAFQIQRIYTKD
        ISFEAPNAPQVFQQDWQPEVKLDL
        DTASSQLAEDVYEVVLRVTVTASLGEETAFLCEV
        QQGGIFSVAGIEGTQLAHCLGAYC
        PNILFPYARECITSLVSRGTFPQLNLAPVNF DAL
        FMNYLQQQAEGEVEGVEQRQDA"
gene      complement(83726..83974 /gene="grxC"
)
CDS      complement(83726..83974 /gene="grxC"
)
        /locus-tag="y0075"
        /function="enzyme; biosynthesis of
        cofactors, carriers: Thioredoxin,
        glutaredoxin, glutathione"
        /note="residues 1 to 82 of 82 are
        78.04 pct identical to residues 1
        to 82 of 83 from E. coli K12 :
        B3610; residues 1 to 82 of 82 are
        85.36 pct identical to residues 1
        to 82 of 83 from GenPept :
        >gb|AAL22561.1| (AE008872)
        glutaredoxin 3 [Salmonella
        typhimurium LT2]"
        /codon-start=1
        /transl-table=11
        /product="glutaredoxin 3"
        /protein-id="AAM83670.1"

```

		/db-xref="GI:21956737" /translation="MAKIEMYTKATCPFCHRAKA LLNAKGAAFHEIAIDNDPAKREEM IARSGRTTVPQIFIDGQHIGGCDDLHALDARGGL DPLL"
gene	complement(84093..84527	/locus-tag="y0076"
)	
CDS	complement(84093..84527	/locus-tag="y0076"
)	
		/note="residues 2 to 144 of 144 are 65.73 pct identical to residues 1 to 143 of 143 from E. coli K12 : B3611; residues 2 to 144 of 144 are 67.83 pct identical to residues 1 to 143 of 143 from GenPept : >gb AAL22562.1 (AE008872) putative Rhodanese-related sulfurtransferases [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83671.1" /db-xref="GI:21956738" /translation="MLQEIMQFISQHPILSLAWV LLFGAVVFTSFKNSLSKVKEVTRG EATRLINKEDAVVVDIRTREDYRKGHIAN SINLI PSDIKNGNLGELEKHKTQPIIVVC AMGTTSRASADMLSKAGFERVFTLKEGISGWSGE NLPLARGK"
gene	84924..86471	/locus-tag="y0077"
CDS	84924..86471	/locus-tag="y0077"
		/note="residues 1 to 515 of 515 are 83.30 pct identical to residues 1 to 514 of 514 from E. coli K12 : B3612; residues 1 to 515 of 515 are 83.88 pct identical to residues 1 to 514 of 514 from GenPept : >gb AAL22563.1 (AE008872) phosphoglyceromutase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="putative 2,3-bisphosphoglycerate-independen t phosphoglycerate mutase" /protein-id="AAM83672.1" /db-xref="GI:21956739" /translation="MSSTKKPLVLTILDGYGHRE EQQDNAILNAKTPVMDVLWQQQPH TLIAASGLDVGLPDGQMGNSEVGHVNLGAGRIVY QDLTRLDKIKEGDFFTNPTLTAA VDNAVKTGKAVHIMGLLSAGGVHSHEDHIMAMVE LAAKRGATAIYLHAFLDGRDTPPR SAESSLKRFTAKFAELGNGRIASIIIGRYAMDRD NRWDRVQLAYDLLTQAKGEFTADN AVAGLQAAYARGENDEFVKPTVIQATGEADAAMN EGDTLIFMNFRAADRARQITRTFVN AEFDGFKRDKVVNFGDFIMLTEYAADIKVACAYP PASLTNTFGEWLMKHDKTQLRISE TEKYAHVTFFYNGGVEEPFKGEDRILINSPKVAT

gene	86481..87851	YDLQPEMSSAELTEKLVSAIGSGK
CDS	86481..87851	YDVIIICNYPNGDMVGHTGDYDAAVKAVETLDNCI
		EQVVAAVKAADGQLLITADHGNAE
		QMRDPATGQAHTAHTSLPVPLIYVGNKAVKAVEG
		GKLSDIAPTMLSLMEMEIPQEMTG KPLFIVE"
		/locus-tag="y0078"
		/locus-tag="y0078"
		/function="putative membrane"
		/note="residues 39 to 456 of 456
		are 63.39 pct identical to
		residues 24 to 427 of 427 from E.
		coli K12 : B3613; residues 40 to
		456 of 456 are 65.70 pct identical
		to residues 25 to 427 of 427 from
		GenPept : >gb AAL22564.1
		(AE008872) paral putative membrane
		protein [Salmonella typhimurium
		LT2]"
		/codon-start=1
		/transl-table=11
		/product="putative membrane
		protein"
		/protein-id="AAM83673.1"
		/db-xref="GI:21956740"
		/translation="MKDRELLAKSITTKDAVSDG
		RESPSLSDKLSRLPWSTLYASVF
		CAGVLLLPFSGQAVEPPVAAKASENKNQLKTLQQ
		DIAEKEKSVQQQKKQRSSLLDQLK
		QQENTISQTSRSLRETQATLAELSKDIASLTTSI
		EKLQNQQSQQQSILSKQLAAAFKQ
		GKHSSLQLILSGEESQRSERILAYFSYLNEARQK
		AIEELKQTRTTLSAEKKMLEQKQN
		QHKALLDEQKAQQQKLEQARIARQKTLTSLEASL
		EKDQQSLAELKLNESRLRDQIAKA
		EREAARAEREAKEAARVREQVKVKEQQAKKTGS
		SYKPSESESLMARTGGLGRPGGQ
		ALWFPVRGNVSHRFGEPLQGELRWKGMVITAPEGS
		EVKAIADGRVLLADWLQGYGLVVV
		IEHGKGDMSLYGYNQSALVNVAQVKAGQPIALV
		GTSGGQGEPSLYFEIRRQGQAVNP QPWLGR"
gene	87875..88809	/locus-tag="y0079"
		/note="disrupted by frameshift"
		/pseudo
gene	complement(88947..89972	/gene="tdh"
)	
		/locus-tag="y0080"
CDS	complement(88947..89972	/gene="tdh"
)	
		/locus-tag="y0080"
		/function="enzyme; degradation of
		small molecules; amino acids"
		/note="residues 1 to 341 of 341
		are 92.08 pct identical to
		residues 1 to 341 of 341 from E.
		coli K12 : B3616"
		/codon-start=1
		/transl-table=11
		/product="threonine dehydrogenase"
		/protein-id="AAM83674.1"
		/db-xref="GI:21956741"
		/translation="MKALSKLKAEEGIWMTDVPQ
		PELGHNDIMIKIRKTAICGTDVHI

		YNWDEWSQKTIPVPMVVGHEYVGEVVAIGQEVKG FNIGDRVSGEGHITCGHCRNCRGG RTHLCRNTVGVGVNRPGSFAEYLVIPAFNAFKIP DNISDELAEIFDPFGNAVHTALSF DLVGEDVLVSGAGPIGIMAAVCKHVGARHVVIA DVNEYRLDLARKMGVTRAVNVSKS NLNDVMTELMTEGFDVGLEMSGAPPAFRSLLNS MNHGGRIAMLGIPPSDMSIDWNQV IFKGLFIKGIYGREMFETWYKMAALIQSGLDLTP IITHRFPIDEFQQGFDAMRSGKSG KVVLSWD"
gene	complement (89982..91223)	/gene="kbl"
CDS	complement (89982..91223)	/locus-tag="y0081" /gene="kbl" /locus-tag="y0081" /function="enzyme; central intermediary metabolism: Pool, multipurpose conversions" /note="residues 20 to 413 of 413 are 84.77 pct identical to residues 5 to 398 of 398 from E. coli K12 : B3617" /codon-start=1 /transl-table=11 /product="2-amino-3-ketobutyrate CoA ligase (glycine acetyltransferase)" /protein-id="AAM83675.1" /db-xref="GI:21956742" /translation="MQLPILEITEMSLPCNKHPF YQQLEQQLDTTTRTEGLYKNERVIT SAQQANIAVADGSRVINFCANNYLGLANHPKLIA AAKAGMDSHGFGMASVRFICGTQD IHKELEHKLASFLGMEDAILYSSCFDANGGLFET LLGPEDAIISDALNHASIIDGVRL CKAKRYRYANNDMTELEAQLKQAKAEGARHIMIA TDGVFSMDGVIANLKRVCDLADEY QALVMVDDSHAVGVIGANGRGTHEYCEVMDRVDI ITGTLGKALGGASGGYTAGRKELV EWLRQRSRPYLFSNSLAPAIVAASIEVLSLLEEG GALRDLWANARLFREKMSAAGFT LAGADHAIIPVMLGEAKLAQDFANALLKEGIYVT GFFFPVVPKGQARIRTQMSAGHTT EQVERAIEAFVRIGKQLNVIA"
gene	91394..92371	/gene="rfaD"
CDS	91394..92371	/locus-tag="y0083" /gene="rfaD" /locus-tag="y0083" /function="enzyme; surface polysaccharides and antigens" /note="residues 16 to 323 of 325 are 83.11 pct identical to residues 1 to 308 of 310 from E. coli K12 : B3619" /codon-start=1 /transl-table=11 /product="ADP-L-glycero-D-mannohep tose-6-epimerase" /protein-id="AAM83676.1" /db-xref="GI:21956744" /translation="MGCGTQPRKLARVNTMIIVT"

		GGAGFIGSNIVKALNNIGYKDILV
		VDNLKDGTKFVNLVDLDIADYMDKEDFVASIVAG
		DDMGDIDAIFHEGACSSSTEWDGK
		YMMDNNYQYSKDILHFCLDRSIPFLYASSAATYG
		GRTDNFIEDRQYEQPLNVYGYSKF
		LFDQYVREILPQADSQICGFRYFNVYGPREGHKG
		SMASVAFHLNNQINAGERPKLFAG
		SENFKRDFIYVGDVADVNLWFWQNGVSGIFNCGT
		GRAESFQAVADAVVDYHQSGPVEY
		IEFPEKLGKRYQAYTQADLTKLRAAGYGKPFKTV
		AEGVKEYLAWLNRSV"
gene	92016..92243	/locus-tag="y0082"
CDS	92016..92243	/locus-tag="y0082"
		/note="residues 5 to 33 of 75 are
		48.27 pct identical to residues 94
		to 122 of 182 from GenPept :
		>dbj BAA11839.1 (D83187) delta
		9-fatty acid desaturase [Yarrowia
		lipolytica]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83677.1"
		/db-xref="GI:21956745"
		/translation="MQVKGLSYSRVAKTLNVISF
		MWVMLLTLICGSGKTAYPVFSTAV
		LAGQSLSRSLMQWWIITKVGQSNSSSLKN"
gene	92390..93466	/gene="rfaF"
		/locus-tag="y0084"
CDS	92390..93466	/gene="rfaF"
		/locus-tag="y0084"
		/function="putative enzyme;
		macromolecule metabolism:
		Lipopolysaccharide"
		/note="lipopolysaccharide core
		biosynthesis; residues 5 to 351 of
		358 are 73.77 pct identical to
		residues 1 to 347 of 348 from E.
		coli K12 : B3620; residues 5 to
		351 of 358 are 78.38 pct identical
		to residues 1 to 347 of 348 from
		GenPept : >gb AAL23754.1 (U52844)
		heptosyltransferase II WaaF
		[Serratia marcescens]"
		/codon-start=1
		/transl-table=11
		/product="ADP-heptose--lps
		heptosyltransferase II"
		/protein-id="AAM83678.1"
		/db-xref="GI:21956746"
		/translation="MINGMKILVIGPSWVGDMMM
		SQSLYRTLKAEYPAADIDVMAPAW
		CRPLLARMPEVRHAIPMPLGHGAFAFEERRRLGL
		ALRETEYDRAYVLPNSFKSALIPY
		FSGIKRRIGWRGEMRYFLLNDRILDKQAFPMMV
		QRYVALAYDKERIRSAADLPQPLL
		WPQLQVRDEEIAETTASFNLTDNRPIIGFCPGA
		FGPAKRWPYHYATLAQKLIDGY
		QVILFGSAKDNEAGEDIRQALSDTDREYCLNLAG
		QTSLEQAVVLIAACSAVVSNDLGL
		MHVAAALNKPLVALYGPSSPDFTPLSEKATVIR
		LITGYHKVRKGDQAQGYHQSILDI

gene	93442..94431	QPEHVMAALEKQLATQECSVKGGD"
		/gene="rfaC"
		/locus-tag="y0085"
CDS	93442..94431	/gene="rfaC"
		/locus-tag="y0085"
		/function="enzyme; macromolecule
		metabolism: Lipopolysaccharide"
		/note="lipopolysaccharide core
		biosynthesis; residues 9 to 327 of
		329 are 68.33 pct identical to
		residues 1 to 319 of 319 from E.
		coli K12 : B3621; residues 9 to
		329 of 329 are 81.30 pct identical
		to residues 1 to 321 of 321 from
		GenPept : >gb AAL23755.1 (U52844)
		heptosyltransferase I WaaC
		[Serratia marcescens]"
		/codon-start=1
		/transl-table=11
		/product="heptosyl transferase I"
		/protein-id="AAM83679.1"
		/db-xref="GI:21956747"
		/translation="MLSQRGRMLMHVLIVKTSSMG
		DVLHTLPALTDAMNAIPGIRFDWV
		VEEGFSQIPSWHPAVDKVIPVAIRWRKNWFGSD
		TRQERCDFKRVVQQRSYDRVIDAQ
		GLIKSAALITRIAKGTKHGPDCKSAREPFASWFY
		NCRHEIDTKQHAVERIRQLFAKSL
		GYDKPESYGDYAIQRFNLNQLPADAGQYLVLHA
		TTRDNKHWPESHWVQLIELVQPTG
		LKIKLPWGAEEHQALRLAEHFPHVEVLPKLSL
		QQVAEVLGAKAVVSVDTGLSHLT
		AALDRPNITLFGPTDPGLIGGYGKNQIAVISEQK
		KMDSLAPTIMARLETILIS"
gene	94743..96128	/gene="kdtA"
		/locus-tag="y0086"
CDS	94743..96128	/gene="kdtA"
		/locus-tag="y0086"
		/function="enzyme; surface
		polysaccharides and antigens"
		/note="residues 37 to 461 of 461
		are 79.76 pct identical to
		residues 1 to 425 of 425 from E.
		coli K12 : B3633; residues 37 to
		461 of 461 are 88.47 pct identical
		to residues 1 to 425 of 425 from
		GenPept : >gb AAC44432.1 (U52844)
		3-deoxy-manno-octulosonic acid
		transferase [Serratia marcescens]"
		/codon-start=1
		/transl-table=11
		/product="3-deoxy-D-manno-octuloso
		nic-acid transferase (KDO
		transferase)"
		/protein-id="AAM83680.1"
		/db-xref="GI:21956748"
		/translation="MNNHGSMWCSALLAGKSLFC
		PDMVLFLLIIHINEIDRMLLRLLYQV
		LLYLIQPLIWLRLLLRSRKAPAYRKRWGERYGFC
		AGKVVAGGIMLHSVSVGETLAAIP
		LVRALRHRYPSLPITVTTMTPTGSESVQSAFGKD
		VHVYLPYDLPGSVNRFLDQVNP

		LVIIMETELWPNLINTLHRRKIPLVIANARLSAR SAAGYKKIGSFIRITILQRITLIAA QNQEDGDRFIELGLKRSQLTVTGSLKFDISVTP LAARAVTLRRQWAPHRPVWIATST HDGEETILLEAHRQLLQQFPTLLLILVPRHPERF GKAVELTQKIGLSYTLRSKGEVPS SSTQVVIGDTMGELMLLYGIADLAFVGGSLVERG GHNPLEAAAAHAIPVLMGPHTFNFK DICAKLEQA EGLITVTDTL SLVKEITVLLTDEDC RLYYGRHAVDVLHENQGALQRLH LLEPYLPQRSH"
gene	96129..96911	/locus-tag="y0087"
CDS	96129..96911	/locus-tag="y0087" /function="enzyme" /note="residues 1 to 256 of 260 are 75.78 pct identical to residues 1 to 256 of 257 from GenPept : >gb AAC44433.1 (U52844) glucosyltransferase [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="lipopolysaccharide core biosynthesis glycosyl transferase" /protein-id="AAM83681.1" /db-xref="GI:21956749" /translation="MGTKKRLSVVMITKNEASLL TDCLASVAWADEIIVLD SGSEDET RALAQQFGAKVYSNINWPGYGKQRQLAQQYASGD YILMLDADERVTPELKIAIESVLL APEEGAVYSCSRRLNFLGRFMRHSGWYPDRVTRL YPHHQYRYNDNLVHESLD SGSAKV IPLAGDLLHLTCRDFFAFQKQLSYAEAWAIQRH QQGKSCSYFAILSHTLGAFSKTWL LRA GFLDGKQGLLLAVVNAQYTFNKYAALWALSH QYQKSEKS"
gene	96908..97387	/gene="kdtB"
CDS	96908..97387	/locus-tag="y0088" /gene="kdtB" /locus-tag="y0088" /note="residues 1 to 159 of 159 are 73.58 pct identical to residues 1 to 159 of 159 from E. coli K12 : B3634; residues 1 to 159 of 159 are 82.38 pct identical to residues 1 to 159 of 161 from GenPept : >gb AAD28804.1 (U52844) phosphopantetheine adenylyltransferase CoaD [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="putative enzyme of lipopolysaccharide synthesis" /protein-id="AAM83682.1" /db-xref="GI:21956750" /translation="MITKAIYPGTDFDPITNGHLD LVTRASAMFSHVILAIADSSSKKP MFTLDERVALAKKVTAPLKNVEVLGFSELMAEFA KKHNNANILVRGLRSVSDFEYEWQL ANMNRHLMFKLESVFLIPSEKWSFISSSLVKEVA RHGGDITPFLPKPVTKALLAKLA"

gene	complement(97393..98202	/gene="mutM"
)	
CDS	complement(97393..98202	/locus-tag="y0090"
)	/gene="mutM"
		/locus-tag="y0090"
		/function="enzyme; DNA -
		replication, repair,
		restriction/modification"
		/note="residues 1 to 268 of 269
		are 79.85 pct identical to
		residues 1 to 268 of 269 from E.
		coli K12 : B3635; residues 1 to
		268 of 269 are 83.70 pct identical
		to residues 1 to 270 of 271 from
		GenPept : >gb AAD28805.2 (U52844)
		Fpg [Serratia marcescens]"
		/codon-start=1
		/transl-table=11
		/product="formamidopyrimidine DNA
		glycosylase"
		/protein-id="AAM83683.1"
		/db-xref="GI:21956751"
		/translation="MPPEVETSRRGIEPYLVG
		QTILYAVVRNARLRWPVSDEILTL
		SDQPVLSVQRRAYLLLELPKGWIIHLMGSGSL
		RVLSEETAAEKHDHVDLVVSNNGKI
		LRYTDPRRFGAWLWAKDLETSNVLAHLGPEPLSD
		EFTAQYLFDKSRNKRTLKIPWLMD
		NKVVVGVGNIYASESLFAAGILPDRAAGSLTDAE
		SVLLVATIKAVLLHSIEQGGTTLR
		DFLQSDGKPGYFAQELQVYGRAGEPCRQCGHP
		IAKHGQRSTFFCRHCQH"
gene	97396..97554	/locus-tag="y0089"
CDS	97396..97554	/locus-tag="y0089"
		/note="residues 25 to 43 of 52 are
		57.89 pct identical to residues
		170 to 188 of 433 from GenPept :
		>emb CAB86066.1 (AL163002)
		putative protein [Arabidopsis
		thaliana]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83684.1"
		/db-xref="GI:21956752"
		/translation="MLAVAAKERAALPVFRYFNG
		MPTLPTWFTRTPIDLQLLREIPWF TIRLQKIT"
gene	complement(98285..98452	/gene="rpmG"
)	
		/locus-tag="y0091"
CDS	complement(98285..98452	/gene="rpmG"
)	
		/locus-tag="y0091"
		/function="structural component;
		ribosomal proteins - synthesis,
		modification"
		/note="residues 1 to 55 of 55 are
		96.36 pct identical to residues 1
		to 55 of 55 from E. coli K12 :
		B3636"
		/codon-start=1

		/transl-table=11 /product="50S ribosomal subunit protein L33" /protein-id="AAM83685.1" /db-xref="GI:21956753" /translation="MAKGVREKIKLVSSAGTGHF YTTTKNKRTKPEKLELKKFDPVVR QHVLYKEAKIK"
gene	complement(98963..99631)	/gene="radC"
CDS	complement(98963..99631)	/locus-tag="y0092" /gene="radC" /locus-tag="y0092" /function="phenotype; Not classified" /note="residues 10 to 222 of 222 are 58.21 pct identical to residues 12 to 224 of 224 from E. coli K12 : B3638; residues 7 to 222 of 222 are 59.72 pct identical to residues 6 to 221 of 221 from GenPept : >gb AAL22588.1 (AE008873) putative DNA repair protein, associated with replication forks [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="DNA repair protein" /protein-id="AAM83686.1" /db-xref="GI:21956754" /translation="MDEWYGQVAPREKLLKYGAA VLTD AELLAIFLRTGIPGMHVMKM AEYLIETFGSLHGLISADYQTLCAHKGIGASKYS QIQ AIGELACRCFSSHLMRESVLL NPGITQKFLQNILSHREREIFLVVFLDNQHRVIR HEEMFTGTISSVEVHPREIVREAL KVNAAALILAHNHPSGKAEPSQADRLITTQVIKA CSLLDIRVLDHLVVGRGECVSFAE RGWL"
gene	99711..101042	/gene="dfp"
CDS	99711..101042	/locus-tag="y0093" /gene="dfp" /locus-tag="y0093" /function="phenotype; DNA - replication, repair, restriction/modification" /note="residues 39 to 442 of 443 are 75.18 pct identical to residues 23 to 429 of 430 from E. coli K12 : B3639; residues 40 to 442 of 443 are 75.12 pct identical to residues 1 to 406 of 407 from GenPept : >gb AAL22589.1 (AE008873) flavoprotein affecting synthesis of DNA and pantothenate metabolism [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="flavoprotein affecting synthesis of DNA and pantothenate

		metabolism"
		/protein-id="AAM83687.1"
		/db-xref="GI:21956755"
		/translation="MRDVSQILRLVASESALIAN
		LFNGYAKISPLTAFIRTIMMTGLS
		GKHIVLGISGGIAAYKSPELVRRRLRDKGADVRVV
		MTHAAKAFIAPLTLQAVSGYPVSD
		DLDPAAEAAMGHIELGKWADLVIIAPATADLLA
		RMAAGMANDLLTTVCLATAAPIAA
		VPAMNQMYRAPATQENLQTLKQGVLLWGPDSG
		SQACGDIGPGRMLDPQEIVALAYN
		HFSAKQDLQHLSVMITAGPTREPLDPVRFISNQS
		SGKMGFAIAQALAARGSNVTLIAG
		PVNLSTPEGVKRIDVITALEMQQAVQKIAQQONI
		FISCAAVADYRAEHVSDEKIKKQG
		DEITLKLKKNPDIVAGVASMAKNRPFVVGFAAET
		QNVVEYARQKLARKNLDLICANDV
		SLAEHGFNSDTNALHLFWSTGEKRLPLSDKYLLS
		QRLIDEIVSRYDEKNRH"
gene	101008..101478	/gene="dut"
		/locus-tag="y0094"
CDS	101008..101478	/gene="dut"
		/locus-tag="y0094"
		/function="enzyme;
		2'-Deoxyribonucleotide metabolism"
		/note="residues 6 to 156 of 156
		are 84.76 pct identical to
		residues 1 to 151 of 151 from E.
		coli K12 : B3640; residues 6 to
		156 of 156 are 85.43 pct identical
		to residues 1 to 151 of 151 from
		GenPept :
		>gb AAG58784.1 AE005591-8
		(AE005591)
		deoxyuridinetriphosphatase
		[Escherichia coli O157:H7 EDL933]"
		/codon-start=1
		/transl-table=11
		/product="deoxyuridinetriphosphata
		se"
		/protein-id="AAM83688.1"
		/db-xref="GI:21956756"
		/translation="MSAVMMKKIDIKILDPRVGN
		EFPLPTYATEGSAGLDLRACLDHA
		VELQPGQTTLPTGLAIHIGDSALAAVILPRSGL
		GKHKGIVLGNLVGLIDSDYQGQLM
		VSVWNRGQQPFTIEPGERIAQMVFPVQAEFNL
		VEDFTDSEGTGGFGHSGRQ"
gene	101600..102196	/gene="ttk"
		/locus-tag="y0095"
CDS	101600..102196	/gene="ttk"
		/locus-tag="y0095"
		/function="putative regulator"
		/note="residues 1 to 198 of 198
		are 83.33 pct identical to
		residues 15 to 212 of 212 from E.
		coli K12 : B3641; residues 1 to
		198 of 198 are 83.83 pct identical
		to residues 1 to 198 of 198 from
		GenPept : >gb AAL22591.1
		(AE008873) putative
		transcriptional regulator

		(TetR/ArcR family) [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="AAM83689.1" /db-xref="GI:21956758" /translation="MAEKENTKRNREEILQALA QMLESSDGSQRITTAKLAANVGVS EAALYRHFPKTRMFDSLIEFIEDSLMSRINLIL QDEKETFNRLRLILLVLGFAERN PGLTRIMTGHALMFEQDRQLQGRINQLFERIEMQL RQVLREKKLRDGGQGFHDEALLAT QLLAFCEGMLSRFVRSEFRYCPTQEFDSRWPLIV AQLQ"
gene	complement(102331..102978)	/gene="pyrE"
CDS	complement(102331..102978)	/locus-tag="y0096" /gene="pyrE" /locus-tag="y0096" /function="enzyme; pyrimidine ribonucleotide biosynthesis" /note="residues 1 to 213 of 215 are 85.91 pct identical to residues 1 to 213 of 213 from E. coli K12 : B3642; residues 1 to 213 of 215 are 85.91 pct identical to residues 1 to 213 of 213 from GenPept : >gb AAL22592.1 (AE008873) orotate phosphoribosyltransferase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="orotate phosphoribosyltransferase" /protein-id="AAM83690.1" /db-xref="GI:21956759" /translation="MKAYQREFIEFALNKQVLKF GEFTLKSGRISPYFFNAGLFNTGL DLAKLGRFYAAALMDCGVEFDLLFGPAYKGIPIA TTTAVALAEEHHERDVPYCFNRKEA KTHGEGGNLVGSPLQGRVMLVDDVITAGTAIRES MEIINAQGATLAGVMISLDRQERG RGEISAIQEVERDYHCKVIAIVTLNDVIRYLEDK PEMAEHLVAVRQYREQYGVTL"
gene	complement(103145..103861)	/gene="rph"
CDS	complement(103145..103861)	/locus-tag="y0097" /gene="rph" /locus-tag="y0097" /function="enzyme; degradation of RNA" /note="residues 1 to 223 of 238 are 88.78 pct identical to residues 1 to 223 of 228 from E. coli K12 : B3643; residues 1 to 238 of 238 are 100.00 pct identical to residues 1 to 238 of

		238 from GenPept :
		>emb CAC88911.1 (AJ414141)
		ribonuclease PH [Yersinia pestis]"
		/codon-start=1
		/transl-table=11
		/product="RNase PH"
		/protein-id="AAM83691.1"
		/db-xref="GI:21956760"
		/translation="MRPADRAAQVRPLTLTRNY
		TKHAEGSVLVEFGDTKVLCTATVE
		EGVPRFLKGQGQGWITA EYGMLPRSTHSRNAREA
		AKGKQGGRTLEIQRLIARSLRAAV
		DLKKLGFEFTITLDCDVLQADGGTRTASISGACVA
		LADALNKLVASGK LKANPMKGLVA
		AVSVGIVKGEALCDLEYVEDSAAETDMNVMMED
		GRMIEVQGTAE GEPFSHEEL LALL
		DLARGGIETIFQAQKAAL E S"
gene	103988..104851	/locus-tag="y0098"
CDS	103988..104851	/locus-tag="y0098"
		/function="phenotype; Not
		classified"
		/note="residues 1 to 287 of 287
		are 87.45 pct identical to
		residues 1 to 287 of 287 from E.
		coli K12 : B3644; residues 1 to
		287 of 287 are 87.80 pct identical
		to residues 1 to 287 of 287 from
		GenPept : >gb AAL22594.1
		(AE008873) putative stress-induced
		protein [Salmonella typhimurium
		LT2]"
		/codon-start=1
		/transl-table=11
		/product="putative alpha helix
		protein"
		/protein-id="AAM83692.1"
		/db-xref="GI:21956761"
		/translation="MIRSM TAYARRDIKGEWGNA
		AWELRSVNQRYLE TYIRLPEQFRS
		LEPVIRERIRSR LTRGKIECHLRFELDANAQSSL
		ILNEKLAKQLVEAGN WVKMQSDEG
		EINPVDILRWPGVMSAEEQDLDAISTELMQALDT
		ALDDFIVSRETEGAALKTLIEQRL
		EGVSAEVVKVRAHMPN ILQWQRERLLNKLEEAQV
		QLENT RLEQELVLMAQRIDVAEEL
		DRLEAHVKETY N I L K K E A V G R R L D F M M Q E F N R E
		SNTLASKSINA E V T N S A I E L K V L I
		EQMREQIQNIE"
gene	105254..105877	/locus-tag="y0099"
CDS	105254..105877	/locus-tag="y0099"
		/note="residues 1 to 181 of 207
		are 74.58 pct identical to
		residues 19 to 199 of 223 from E.
		coli K12 : B3646; residues 1 to
		181 of 207 are 74.58 pct identical
		to residues 19 to 199 of 223 from
		GenPept :
		>gb AAG58790.1 AE005592-1
		(AE005592) orf, hypothetical
		protein [Escherichia coli O157:H7
		EDL933]"
		/codon-start=1

		/transl-table=11 /product="hypothetical protein" /protein-id="AAM83693.1" /db-xref="GI:21956762" /translation="MLLSVLYIIGITAEAMTGAL AAGRRQMDMFGVIIIASATAIGGG SVRDMLLGHYPLGWVKHPEYIVIVAIAAIVTTWM APLMKQLRHLFLVLDAIGLIVFSI IGAQIALDMGHSTIIAAIAAVITGVFGGVLRDML CNCIPLVFQKEIYAGISFAAAWIY IALQYTPLSHNWVIIITLITGLALDYSFYDSGLA CLYSNMSTQTIKL"
gene	complement(105890..1075 93)	/locus-tag="y0100"
CDS	complement(105890..1075 93)	/locus-tag="y0100" /note="residues 6 to 564 of 567 are 43.79 pct identical to residues 3 to 561 of 562 from E. coli K12 : B3647" /codon-start=1 /transl-table=11 /product="putative enzyme" /protein-id="AAM83694.1" /db-xref="GI:21956763" /translation="MNILNLKIIMFLLISNTIVV GGAWATSTCPDWPATRIAVEINAL EQQLNKWSAAYHQGHSPVTDDIYDQLQDKLRVW QSCRGLPDKTESQPIPGKGQFLHP VAHTGLKKLKDETALTRWMAGRKNLWVQPKVDGV AVTLVYHGGKLVQLLSRGNGVKGQ NWTEKAPFISAIPQYIANAPALLTLQGELFLLMD GHQQAKSGGVNARSTVAGALMRKS PSPLLAQVGVIWAWPDGPTTMKEKVALQVMGF PFTAKYSEPVMSHLDVVQWRQFWF QAPLPFVTDGVVVRQEEEPAGRYWQATPGQWSMA WKYPPLQHIAEVKDIHFTLGRTGK GTVVLEVLPIKIDDKWIRRVNIGSVTRWKQWDIA PGDHITLALAGHGIPRLDNVVRV HQRNTITAPNWDKFHQLSCFQRLPHGCEPQFLSR LIWLSGPGGLDIGGIGGGFWQELI HHELINDLVGWLLLTPEQIASIPGIGNARAEEKIY QQFQRAKQQPFSRWLLALGFPQVV SVDAQWQVVLRRSLSEWATMAGIGQMRKQIKHF LDHPDVQALADFLSTQKVVGFEFT E"
gene	107994..108617	/gene="gmk"
		/locus-tag="y0101"
CDS	107994..108617	/gene="gmk" /locus-tag="y0101" /function="enzyme; purine ribonucleotide biosynthesis" /note="residues 1 to 207 of 207 are 87.92 pct identical to residues 1 to 207 of 207 from E. coli K12 : B3648" /codon-start=1 /transl-table=11 /product="guanylate kinase" /protein-id="AAM83695.1" /db-xref="GI:21956764" /translation="MVQGTLYIVSAPSGAGKSSL IQALLKTQPLYDTQVSISHTTRAK

		RPGENHGEHYFFVSEKEFCQMIDDDAFLEHAKVF ENYYGTSRLAIEQVLATGVDVFLD IDWQGAQQIRAKMPTARSIFILPPSKTELDRRLR GRGQDSEEVIAKRMEQAVAEMAHY AEYDYLIVNDDFNLALSDLKTIIRAERLRLGRQK QRHDALISKLLAD"
gene	108672..108947	/gene="rpoZ"
		/locus-tag="y0102"
CDS	108672..108947	/gene="rpoZ"
		/locus-tag="y0102"
		/function="enzyme; RNA synthesis, modification, DNA transcription"
		/note="residues 1 to 91 of 91 are 92.30 pct identical to residues 1 to 91 of 91 from E. coli K12 : B3649"
		/codon-start=1
		/transl-table=11
		/product="RNA polymerase, omega subunit"
		/protein-id="AAM83696.1"
		/db-xref="GI:21956765"
		/translation="MARVTVQDAVEKIGNRFDLV LVAARRARQIQSGGKDALVPEEND KVTVIALREIEEGLITNQILDVRERQEQEQQAA EIQAVTAIAEGRR"
gene	108967..111075	/gene="spoT"
		/locus-tag="y0103"
CDS	108967..111075	/gene="spoT"
		/locus-tag="y0103"
		/function="enzyme; global regulatory functions"
		/note="residues 1 to 702 of 702 are 91.45 pct identical to residues 1 to 702 of 702 from E. coli K12 : B3650; residues 1 to 702 of 702 are 91.89 pct identical to residues 1 to 703 of 703 from GenPept : >gb AAL22601.1 (AE008874) bifunctional : (p)ppGpp synthetase II; also guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase [Salmonella typhimurium LT2]; guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase"
		/codon-start=1
		/transl-table=11
		/product="(p)ppGpp synthetase II"
		/protein-id="AAM83697.1"
		/db-xref="GI:21956766"
		/translation="MYLFESLNLLIQRYLP EEQI KRLKQAYLVARDAHEGQTRSSGEP YITHPVAVACILAEMRLDYETLMAALLHDVIEDT PATYQDMEQLFGKSVAELVEGVSK LDKLNFRDKKEAQAENFRKMIMAMVQDIRVILIK LADRTHNMRTLGLSLRPDKRRRIAR ETLEIYSPLAHLRGIHHLKTELEELGFEALYPNR YRVIKEVVKAARGNRKEMIQKILA EIEGRLTEAGIPCRVSGREKHLYSIYCKMHLKEQ RFHSIMDIYA FRVIVKEVDTCYRV LGQAHS LYKPRPGRVKDYIAIPKANGYQSLHTSL

		IGPHGVPVEVQIRTEDMDQMAEMG VAAHWAYKEQGEGSTTAQIRAQRWMQSLLLELQQS AGSSFEFIESVKSDLFPDEIYVFT PEGRIVELPAGATPVDFAYVVHTDIGHACVGARV DRQPYPLSQPLSSGQTVEIITAPG ARNAAWLNFBVSSKARAKIRQLLKNLKRDESVS LGRLLNHALGNRKLSDISEENI KHELDRLMLATVDDLLAEIGLGNAMSVVAKNLL GDPSTLGTASGTRKLPKADGV LITFAKCCRPIPGDPIIAHISPGKGLVIHHESCR NIRGYQKEPEKFMAVEWDQETEQE FIAEIKVDMFNQQGALANLTAAINAAESNIQSLN TEEKDGRVYSAFIRLTTRNRVHLA NIMRKIRIMPDVVKVSRNRN"
gene	111081..111773	/gene="spoU"
		/locus-tag="y0104"
CDS	111081..111773	/gene="spoU"
		/locus-tag="y0104"
		/note="residues 1 to 227 of 230 are 82.81 pct identical to residues 1 to 227 of 229 from E. coli K12 : B3651"
		/codon-start=1
		/transl-table=11
		/product="putative RNA methylase"
		/protein-id="AAM83698.1"
		/db-xref="GI:21956767"
		/translation="MNPQRYARICDMLATRQPD LTVCLEQVHKPHNVSAIIRTADAVG IHQVHAIWPTTQMYTRLSAAAGSNSWVQVKTHP HIAIAIYLKSQDMQILATHLSDKA VDFREIDYTRPTCILMGQEKTGISPEALALADQD IIIPMIGMVQSLNVSVASALILYE AQRQRQNAGMYKRTHSVLAESEQQRLLFEGGYPV LAHVAKRKGLPQPHIDEQQGQIIAD AQWWSAMQATES"
gene	111774..113855	/gene="recG"
		/locus-tag="y0105"
CDS	111774..113855	/gene="recG"
		/locus-tag="y0105"
		/function="enzyme; DNA - replication, repair, restriction/modification"
		/note="resolution of Holliday junctions, branch migration; residues 1 to 693 of 693 are 81.52 pct identical to residues 1 to 693 of 693 from E. coli K12 : B3652; residues 1 to 693 of 693 are 81.24 pct identical to residues 1 to 693 of 693 from GenPept : >gb AAL22603.1 (AE008874) DNA helicase, resolution of Holliday junctions, branch migration [Salmonella typhimurium LT2]"
		/codon-start=1
		/transl-table=11
		/product="DNA helicase"
		/protein-id="AAM83699.1"
		/db-xref="GI:21956768"
		/translation="MKGRLLDAVPLSTLSGVGAS QAGKLAKIGLETIQDLLLHLPLRY"

EDRTRLYRIGDLLPGLSVTVEGEVLRSDISFGRR
 RMMTCQISDGSGLTLRFFNFNAA
 MKNSLSVGKHVIAYGEAKRGNGPEIIHPEYRVH
 GENIGVELQESLTPVYPTTEGIRQ
 ATLRLKIDQALAMLDTCVIAELLPIELSRSLISL
 PEAHTLHRPPADIQLADLEQGKH
 PAQRLIMEELLAHNLSMLAVRAGAQSRYALPLM
 AEEQLKQRFLLAALPFTPTQAQQRV
 VAEIERDMTQSFPMRLIQGDVGSGKTLVAALAA
 LRAIAHGKQVALMAPTELLAEQHA
 TTFRQWLEPLGFSVGWLAGKQKGLARLAQQEAVA
 SGQVSMVIGTHAMFQEQQVQFSGLA
 LVIIDEQHRFGVHQRLTLWEKGEEQGFHPHQLIM
 TATPIPRTLAMTAYADLDTSTVIDE
 LPPGRTPVTTVAIPDTRSDVIQRVKNACLEEGR
 QAYWVCTLIEESELLEAQAAEVTC
 EELKIALPEIKVGLVHGRMGPEKQAIMLAFKQG
 ELQLLVATTVIEVGVDVFNASLMI
 IDNPERLGLAQLHQLRGRVGRGAVASHCVLLYKT
 PLSKTAQMRLQVLRDSNDGFVIAQ
 RDLEIRGPGELLGTRQTGSAEFKVADLLRDQAMI
 PEVQVRVARHLHQQYPEHAKALIER
 WLPERVRYTNA"

gene	complement (114221..1154 35)	/gene="gltS"
CDS	complement (114221..1154 35)	/locus-tag="y0106" /gene="gltS" /locus-tag="y0106" /function="transport; transport of small molecules; amino acids, amines" /note="residues 1 to 399 of 404 are 82.45 pct identical to residues 1 to 399 of 401 from E. coli K12 : B3653; residues 1 to 399 of 404 are 82.45 pct identical to residues 1 to 399 of 401 from GenPept : >emb CAA06485.1 (AJ005339) glutamate permease [synthetic construct]" /codon-start=1 /transl-table=11 /product="sodium/glutamate symporter" /protein-id="AAM83700.1" /db-xref="GI:21956770" /translation="MFHLDTYGTLVAACLVLLLG RKLVTVPFLKKYTIPEPVAGGLL VAFMMLLVQKTLGWEVSFDMSLKDPLMLAFFATI GLNANLASLRAGGKALSIFVFIVV GLLLVQNTIGIVLAKLMGLDPLMGLLAGSITLSG GHGTGAAWSKLFSERYGFENATEV AMACATFGLVLGGLIGGPVARYLVKHSSTPEGTP DDSAVPSAFEKPSAGRMITSLVLI ETIAMISICLMAGNLIAGWLQGTMFELPIFVCVL FVGVLSTNTLSASGFYRVFDRAVS VLGNVSLSLFLAMALMSLKLWELASLALPMLVIL SVQALAMALYAI FVTYRIMGKNYD AAVLAAGHCGFGLGATPTAIANMQAITDRFGPSH LAFLVPMVGAF FIDIVNAIVIKL YLLLP I FPAVTG"

gene	115622..117058	/locus-tag="y0107"
CDS	115622..117058	/locus-tag="y0107"
		/function="putative transport"
		/note="residues 18 to 478 of 478 are 83.98 pct identical to residues 1 to 462 of 463 from E. coli K12 : B3654; residues 18 to 478 of 478 are 83.76 pct identical to residues 1 to 462 of 463 from GenPept : >gb AAL22606.1 (AE008874) putative NCS2 family, purine/xanthine transport protein [Salmonella typhimurium LT2]"
		/codon-start=1
		/transl-table=11
		/product="putative transport protein, symporter"
		/protein-id="AAM83701.1"
		/db-xref="GI:21956771"
		/translation="MSRIIKMPPLPIWKYHAMST QSAELDTAPPSPAHPSELIYHLED RPPLPQTLFAACQHLLAMFVAVITPGLLICQALG LPAEDTQRIISMSLFASGLASLLQ IKTWGPVGSGLLSIQGTSFNFVSPLIMGGLALKN GGADIPTMMAALFGTLMVASCTEI LLSHVLHLARRIITPLVSGIVVMIIGLSLIQVGL TSIGGGYGAMSDNTFGAPKNLLLA GAVLGVIILLNRQRNPYLRVASLVIAMAVGYLLA WALGMLPESRPVVD TALIT IPTPL YYGLSFDWNLLIPLMLIFMVT SLETIGDITATSD VSEQPVRGPLYMKRLKGGVLANGL NSMLSAIFNTFPNSCFGQNNGVIQLTGVASRYVG FVVAIMLIILGLFPAVAGFVQHIP EPVLGGATLVMFGTIAASGVRIVSRET LNRR AIM IMALSLAVGMGVAQQPLILQFAPD WIKTLFSSGIAAGGITAIVLNLLFPQEK"
gene	117206..118915	/locus-tag="y0108"
CDS	117206..118915	/locus-tag="y0108"
		/note="residues 1 to 563 of 569 are 49.02 pct identical to residues 1 to 557 of 569 from E. coli K12 : B3655"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83702.1"
		/db-xref="GI:21956772"
		/translation="MKFLGKTLTLLLLFALSIV LCYAVLQTSWAAGWLSRWVSNNSG YHLSLRGIDHRWSQPGQISFSDVTLARADQPPFL TAQQVIFGLSWRQLTDPKHFLSLQ LQNGSLTLNNSTPSLPLQADTLQLTDMTLNTTVE SKNATSQWKIAGQHVNGGLVPWQP IPGNSFGENTQFHFSAGFLTINDISAQQIYLQGS IQKDILTLTNFGANIAQGELTGNA RQSADGSWLVDRLRLSNIRLQTTASLEDVWNNVL QLPPITLKRFDLIDARVEGKGWAV NDVDLTLKNITFKQGDWQSDDGELVFNASDIIKG NIHLIDPIATFTLSPEGVAINQFT TRWQDGLLRTLGSWSRATHRLQLGELTVVALVYT LPNDWKQLWQQTLPDWLSEVYVGK LSANRNLLIDISPDPFQITSLDAAGSNLLLAKN"

		HQWGVWSGSLVLNAGNATFNKNDI RRPSLALNANEQQITFSDLRAFTKEGLLEATASI DQTPDRALSLALTGRSVDLNLFLHN WGWPALPLQGLGNLKLQIKGNLTADAPLKPTLNG SLQAIDSNGQQINQTVLHGVVQGT AEQ"
gene	complement(119050..119973)	/locus-tag="y0109"
CDS	complement(119050..119973)	/locus-tag="y0109"
		/note="residues 1 to 298 of 307 are 83.89 pct identical to residues 17 to 314 of 329 from E. coli K12 : B3888" /codon-start=1 /transl-table=11 /product="putative acetyltransferase" /protein-id="AAM83703.1" /db-xref="GI:21956773" /translation="MYHLRVPITEQELKDYYQFR WEMLRKPLHQPIGSEKDAYDAMAH HQMVVDEQ GKAVAIGRLYINADNEAAIRFLAVAP SVRNKGLGTLVAMTLESVARQEGV KRVVCSAREDAVDFFAKLGFVCQGEITAPQTTTPV RHFLMIKPVATMDDILHRPDWCGQ LQQAWYDHIPLSEKMGVRISQYTGQRFVTTMPEA GNQNPHTLTFAGSLFSLATLTGWG LIWLLLRERHLGGTIILADAHIRYSAPVTGRPRA VAELSSLSGDLRLARGRRARVQL NVNLFGDENQGAVFEGTYMVLPAAGDDMAN"
repeat-region	120157..122106	/note="insertion element" /insertion-seq="IS100"
gene	120608..121261	/locus-tag="y0110"
CDS	120608..121261	/locus-tag="y0110"
		/function="IS and transposon related functions" /note="IS100; orfA; residues 1 to 217 of 217 are 100.00 pct identical to residues 124 to 340 of 340 from GenPept : >gb AAC13168.1 (AF053947) putative transposase [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83704.1" /db-xref="GI:21956774" /translation="MQVDWGTMRNGRSPLHVFVA VLGYSRMLYIEFTDNMRYDTLETC HRNAFRFFGGVPREVLVDNMKTVVLQRDAYQTGQ HRFHPSLWQFGKEMGFSPRLCRPF RAQTKGKVERMVQYTRNSFYIPLMTRLRPMGITV DVETANRHGLRLWHDVANQRKHET IQARPCDRWLEEQQSMLALPPEKKEYDVHLDENL VNFDKHPLHHPLSIYDSFCRGVA"
gene	121258..122040	/locus-tag="y0111"
CDS	121258..122040	/locus-tag="y0111"
		/function="IS and transposon related functions" /note="IS100; orfB; residues 1 to 260 of 260 are 100.00 pct

		<p>identical to residues 1 to 260 of 260 from GenPept : >gb AAC69770.1 (AF074612) putative transposase [Yersinia pestis]"</p> <p>/codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83705.1" /db-xref="GI:21956775" /translation="MMMELQHQRMLMALAGQLQLE SLISAAPALSQQAVDQEWSYMDFL EHLLEHEKRLARHQKQAMYTRMAAFPAVKTFEEY DFTFATGAPQKQLQSLRSLSFIER NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF TTAADLLLQLSTAQRQGRYKTTLQ RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIKR YEKSAMILTSNLPFGQWDQTFAGD AALTSAMLDRLHSHVQIKGESYRLRQKRKAG VIAEANPE"</p>
gene	122056..122991	/locus-tag="y0112"
CDS	122056..122991	<p>/locus-tag="y0112" /note="residues 18 to 310 of 311 are 77.81 pct identical to residues 35 to 327 of 328 from E. coli K12 : B3102" /codon-start=1 /transl-table=11 /product="putative transferase" /protein-id="AAM83706.1" /db-xref="GI:21956776" /translation="MGRWWRYKWITFHPSLTSTD GQAGPQKGKGFNAEAHRYHLYVSL ACPWAHRALLMRTLKGLSLSVSVVHPLMQENG WTFSSDFPAATGDALYHLDYLYQL YLRAAPDYSGRVTVPVLWDKQQQTVVSNEADII RMFNNAFDDVGAKAGDYYPALRN DIDDINGWVYDQVNNGVYKAGFATTQEAYDEAVG TLFSALDRLEQILGQHRYLTGNQL TEADLRLWTTLVRFDPVYVTHFKCDKRRISDYPN LYGFLRDIYQMPGIAETVDFAHIR THYYRSHGTINPYGIISIGPQQNLLEPHDRANRF V"</p>
gene	complement(123122..124015)	/locus-tag="y0113"
CDS	complement(123122..124015)	<p>/locus-tag="y0113" /function="putative regulator" /note="residues 1 to 294 of 297 are 89.45 pct identical to residues 1 to 294 of 298 from E. coli K12 : B3105" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator LYSR-type" /protein-id="AAM83707.1" /db-xref="GI:21956777" /translation="MARDRALTLALRVMDAIDR RGSFAAADELGRVPSALSMTQK LEEELDVVLFDRSGHRTKFTNVGRMLLERGRVLL EAADKLTTDAEALARGWETHITIV SEALSPAOKLFPLIDKLALKANTQVSILTEVLG</p>

		AWERLEQGRADIVIAPDMHFRASS EINSRKLYKVTSVYVASPDHPIHQEPEPLSELTR VKYRGIAVADTARERPVITVQLLD KQQRLTVSTIEDKRRALLAGLG VATMPYEMVEKD IAAGRLRVIGPEYSREADIIMAWR RDSMGEAKSWCLREIPKLLGK"
gene	complement(124135..124284)	/locus-tag="y0114"
CDS	complement(124135..124284)	/locus-tag="y0114"
		/codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83708.1" /db-xref="GI:21956779" /translation="MIMTMITSYTGHLSSHRKES VGLSIGSPLQDCGNRFSTRLSFVG RFPES"
gene	124277..124981	/locus-tag="y0115"
CDS	124277..124981	/locus-tag="y0115"
		/note="residues 1 to 234 of 234 are 68.80 pct identical to residues 1 to 233 of 233 from E. coli K12 : B3106; residues 1 to 234 of 234 are 71.79 pct identical to residues 1 to 233 of 233 from GenPept : >emb CAD07760.1 (AL627278) conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83709.1" /db-xref="GI:21956780" /translation="MITCRTAEQCGQADFGWLQA RYTFSFGHYFDPTLLGYASLRVLN QEV LAPGAAFPRTYPQVDILNLILQGEAEYRDS LGNHVHAKTGDALLFSPQQGVSY EHNLSANKSLTRIQLWLNACPERESAPTQHQRLS TRPVQLLASPAGEQGSLLRQQMW IHHLALAAGEQQKMPLHGHAYLQSIHGTVDATG PQTGTSQRLTCGDGAFVEEQHLV IKAITPLRALLIDLVP"
gene	complement(125522..125898)	/locus-tag="ys001"
misc-RNA	complement(125522..125898)	/locus-tag="ys001"
		/product="RNase P, RNA component" /note="M1 RNA; processes tRNA" /function="RNA; Macromolecule degradation: Degradation of RNA"
gene	125522..125890	/locus-tag="y0116"
CDS	125522..125890	/locus-tag="y0116"
		/note="residues 82 to 114 of 122 are 48.48 pct identical to residues 47 to 79 of 271 from GenPept : >dbj BAB31852.1 (AK019785) data source:SPTR, source key:Q9NQV8, evidence:ISS homolog to PR-domain containing protein 8 putative [Mus musculus]" /codon-start=1

		/transl-table=11 /product="hypothetical" /protein-id="AAM83710.1" /db-xref="GI:21956781" /translation="MELTGKPGSVVDSHSSRP AHWLKQPTRVQYGPYHNPYLALL RVEFTMPRTVASRAVRSYRTLSPDPDTCVGHRR FALCCTCRRLAPPRRYLAPCPMEP GLSSPPPVSPERDGSEAATV"
gene	complement(125918..126817)	/locus-tag="y0117"
CDS	complement(125918..126817)	/locus-tag="y0117"
		/note="residues 1 to 286 of 299 are 85.31 pct identical to residues 1 to 285 of 286 from E. coli K12 : B3146" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83711.1" /db-xref="GI:21956782" /translation="MNQHRAVISASTLYVVPTP IGNLGDITHRALEVLKGVDLIAAE DTRHTGLLLLQHFAINARLFALHDHNEQQKADQLL AKLQEGQSIALVSDAGTPLINDPG YHLVRRCREAGIRVVPLPGACAAITALSAAGLAS DRFCYEGFLPAKTKGRKDTLQALI EEPRTLIFYESTHRLLESQDMVTVLGPQRYVVL ARELTKTWESIHGAPVGELLAWVK EEETRRLRGEMVLIVEGHKVQSDDALPADALRTLA LLQKELPLKKAALAAEIHGVKKN ALYKYALEQQQGDVETEEDDIQQ"
gene	126784..128853	/locus-tag="y0118"
CDS	126784..128853	/locus-tag="y0118"
		/note="residues 33 to 689 of 689 are 53.00 pct identical to residues 1 to 678 of 678 from E. coli K12 : B3147; residues 33 to 687 of 689 are 55.99 pct identical to residues 1 to 678 of 680 from GenPept : >gb AAL22136.1 (AE008850) paral putative transglycosylase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="putative glycosylase" /protein-id="AAM83712.1" /db-xref="GI:21956783" /translation="MQKLLDRVDSLPHPNYRFN IEHLEKNITGYSMLSSTFVRSKAG LVPVILAAALILAACTGDAPQTPPPVNIQDEASAN SDYYLQQQLQQSSDDNKADWQLLAI RALLREAKVPQAAEQLSTLPANLSDTQRQEQQLL AAELLIAQKNTPAADILAKLEAT QLSANQKVRYYYQAQIAANQDKATLPLIRAFIAQE PLLTDKAHQDNIDGTWQSLSQLTP QELNTMVINADENVLQGWLDLLRVYQDNKQDPEL LKAGIKDWQTRYPQNPAAKNLPTA LTQISNFSQASTAKIALLLPLSGPAQVFADAIQQ GFTAAQNGSAVTASVPVTPNVTES

		SPTDTAAVVSDDTPATLPAPVPPPVTNAQVKIY DTNTQPLAALLAQAQQDGATLVVG PLLKPEVEQLSATPSTLNILALNQPEASNNSPNI CYFALSPEDEARDAHHHLWEQQR MPLLLVPRGALGERIAKAFADWQKQGGQTVLQQ NFGSTTELKQS INSGAGIRLTGTP VSVSNVAAAPASVTIAGLTIPAPPIDAPVVSTSS SGNIDAVYIIIATPSELTLIKPMID MATSSRSKPALFASSRSYQAGAGPDYRLEMEGIQ FSDIPLMAGSNPALLQQASAKYAN DYSLVRLYAMGIDAWALANHFSEMRQIPGFQVKG VTGDLTASSDCVITRKLPLWLQYRQ GMVVPLA"
gene	128937..129290	/locus-tag="y0119"
CDS	128937..129290	/locus-tag="y0119" /note="residues 1 to 115 of 117 are 57.39 pct identical to residues 14 to 128 of 131 from E. coli K12 : B3148; residues 1 to 115 of 117 are 57.39 pct identical to residues 14 to 128 of 131 from GenPept : >gb AAL22137.1 (AE008850) putative endonuclease [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83713.1" /db-xref="GI:21956784" /translation="MSQRDTGAHYENLARRHLER AGLVFQAANVAFRGGEIDLIMRDG DAWVFVEVFRNRNDLFGGAAASITPRKQQRHLA AAVWLAQRGASFATTSCRFDVVAI TGNQLEWLPNAFNTD"
gene	complement(129011..129391)	/locus-tag="y0120"
CDS	complement(129011..129391)	/locus-tag="y0120" /note="residues 3 to 49 of 126 are 37.99 pct identical to residues 674 to 722 of 1684 from GenPept : >gb AAC27151.1 AAC27151 (AC004512) Similar to gb U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb T42908, gb AA586170 and gb AA395125 come from this gene. [Arabidopsis thaliana]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83714.1" /db-xref="GI:21956785" /translation="MLFKLVDPDQFFSRLPSACNS NYLGIARYQLENKHQSVLKALGSH SNWLPVIATTSKRQDVVAKLAPRCASQTAAARCS RCCLRGVILAAAPPNRSRLRRKRTS TNTHASPSRIIRSISPPRKATLAA"
gene	complement(129415..129501)	/locus-tag="y0121"
CDS	complement(129415..129501)	/locus-tag="y0121" /note="residues 2 to 25 of 28 are

		50.00 pct identical to residues 839 to 862 of 1165 from GenPept : >gb AAD10500.2 (U53471) receptor tyrosine kinase proto-oncogene [Xiphophorus xiphidium]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83715.1"
		/db-xref="GI:21956786"
		/translation="MVTLNPNHLLVVDFKVS KLIGINEPYP"
gene	129561..130151	/locus-tag="y0122"
CDS	129561..130151	/locus-tag="y0122"
		/note="residues 1 to 196 of 196 are 93.36 pct identical to residues 1 to 196 of 196 from E. coli K12 : B3149"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83716.1"
		/db-xref="GI:21956787"
		/translation="MLERIKGCFTESIQTQIAAA EALPDAISCAAMALVQSLLNGNKI LCCGNGTSAANAQHFASMINRFETERPSLPAIA LNADNVVLTAITNDRHLHDEVYAKQ VRALGQAGDVLLAISTRGNSRDIVKAVEAAVTRD MTIVALTG YDGGELAGLLGQLDVE IRIPSHRGARVQELHMLTVNCLCDLIDNTLFPHQ ND"
gene	130117..130737	/locus-tag="y0123"
CDS	130117..130737	/locus-tag="y0123"
		/function="putative transport"
		/note="residues 16 to 206 of 206 are 73.29 pct identical to residues 1 to 191 of 191 from E. coli K12 : B3150; residues 16 to 206 of 206 are 73.82 pct identical to residues 1 to 191 of 191 from GenPept : >gb AAL22139.1 (AE008850) paral putative periplasmic protein [Salmonella typhimurium LT2]"
		/codon-start=1
		/transl-table=11
		/product="conserved putative exported protein"
		/protein-id="AAM83717.1"
		/db-xref="GI:21956788"
		/translation="MTTLYFLIRTIKGAPMKVGY IFAMLFSTLLLQGCVGAVVVSAA VATKTATDPRTIGTQVDDGTLEARVVNALS KDKEIKSQTRFVVTAYQGKVLITGQTPS AELSNRAQIASGV DGVTEVYNEMRLGKPV DLSTASMDTWITTKVRSQLLTSDSVKSS NVKVTTENGEVFLGLVTQQEAQSAQIASKV SGVKHVTTAFTIVK"
gene	complement(130944..131669)	/gene="mtgA"
		/locus-tag="y0124"
CDS	complement(130944..131669)	/gene="mtgA"

69)

```
/locus-tag="y0124"
/note="residues 17 to 241 of 241
are 72.44 pct identical to
residues 18 to 242 of 242 from E.
coli K12 : B3208"
/codon-start=1
/transl-table=11
/product="putative peptidoglycan
enzyme"
/protein-id="AAM83718.1"
/db-xref="GI:21956789"
/translation="MISVRRGFSQLWYWGKRGVI
GIIALWMAGILIFAFLPVPFSMVM
IERQLGAWLTGDFAYVAHSDWVPMDEISPYMALA
VMAAEDQKFPDHWGFDVGAIESAL
SHNQNRNQKRIRGASTLSQQTAKNVFLWDGRSWVR
KGLEVGLTAGIELIWTKRRLTVY
LNIAEFGNGIFGVEAAARHFFNKPASKLSASEAA
LLAAVLPNPLRFKVNAPSGYVISR
QQWILRQMHQLGGKTFLQENTLD"
gene      complement(131666..1323 /locus-tag="y0125"
19)
CDS      complement(131666..1323 /locus-tag="y0125"
19)
/function="putative factor"
/note="residues 1 to 217 of 217
are 63.59 pct identical to
residues 4 to 220 of 220 from E.
coli K12 : B3209; residues 1 to
217 of 217 are 65.89 pct identical
to residues 1 to 217 of 217 from
GenPept : >emb|CAD07844.1|
(AL627278) conserved hypothetical
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="sigma cross-reacting
protein 27A (SCR-27A)"
/protein-id="AAM83719.1"
/db-xref="GI:21956790"
/translation="MKTVGCVLSGCGVLDGAEIH
ESVLTMLALDRAGAEVLFFAPDKP
QLHVINHITGEIVAEERNVLVESARIARGLITPL
SAADPEVLDALIVPGGFGAANKLC
DFAIKGGECVSEPDLYKLIQLMHKSGKPIGLMCI
SPVMLPKLLGKPIRLTIGNDPDTI
DAIEIMGGEHVICPADDDVIDLENKVVTTPAYML
AGSISEAAKGIDKLVTKVLDLTE"
gene      complement(132561..1348 /gene="arcB"
97)
CDS      complement(132561..1348 /gene="arcB"
97)
/locus-tag="y0126"
/function="enzyme; global
regulatory functions"
/note="sensor for arcA; residues 1
to 778 of 778 are 75.92 pct
identical to residues 1 to 776 of
776 from E. coli K12 : B3210;
```

residues 1 to 778 of 778 are 77.33
 pct identical to residues 1 to 778
 of 778 from GenPept :
 >gb|AAL22197.1| (AE008853) sensory
 histidine kinase in two-component
 regulatory system with ArcA,
 senses redox conditions
 [Salmonella typhimurium LT2]"
 /codon-start=1
 /transl-table=11
 /product="aerobic respiration
 sensor-response protein; histidine
 protein kinase/phosphatase"
 /protein-id="AAM83720.1"
 /db-xref="GI:21956791"
 /translation="MKQIRVLAQYYVDLMVKLGL
 VRFSLLLASALVLLAMVVQMAVTF
 VLRGSVETLDLVRISFFGLLITPWAVYFLSVVVE
 QLEESRQRLSRLVDKLEVMRHRDL
 ELNKQLTENITQLNQEIVEREKAEKAHLQVVDKL
 KEEMGHREQAQIELGQQSALLRSF
 LDASPDLVYYRNEDNEFSGCNRAPELLTGKSEKQ
 LVGLTPKDVYAPDIAEKVMETDEK
 VFRHNVSLTYEQWLVPDGRKACFELRKVPFYDR
 VGKRHGLMGFGRDITERKRYQDAL
 ENASRDKTTFISTISHELRTPLNGIVGLSRILLD
 TELDAEQLKYLKTIHVSAITLGNL
 FNDIIEMDKLERRKVQLDNQPVDFTGFMADLENL
 SGLLVQPKGLKFIMEPQLPLPEKV
 IADGTRLRQILWNLIGNAVKFTQQGKIVVRVRE
 GNDRLIFEVEDSGMGIPEDQDKI
 FAMYYQVKDRNGGRPATGTGIGLAVSKRLAQSMG
 GDITVKSTQGVGSCFTLTIKAPAV
 QEASNAPSGDDMPLPALHVLLVEDIELNVIVARS
 VLEKLGNSVDVAMNGHDALAMFNP
 EDFDLVLLDIQLPDMSGLDIARQIRAEYQKQSLP
 PLVALTANVLKDKKEYLDAGMDDV
 LSKPLSVPALTAMIKQFWDSPSSAVQKQEHKVM
 QTHESLLDTTMLEQYIDLVGQQLI
 HQSLEMFEQMMPGYLAVLDSNMTARDQKGITEEA
 HKIKGAAGSVGLRHIQQLAQQIQT
 PTLPAWWDNVQDWVDELKLEWRNDVQVLEWAAE
 VEKK"

gene complement(135161..1361 /locus-tag="y0127"
 50)

CDS complement(135161..1361 /locus-tag="y0127"
 50)

/note="residues 23 to 323 of 329
 are 78.73 pct identical to
 residues 1 to 301 of 309 from E.
 coli K12 : B3211"
 /codon-start=1
 /transl-table=11
 /product="hypothetical protein"
 /protein-id="AAM83721.1"
 /db-xref="GI:21956793"
 /translation="MLLGRNANGFGYGLFLTGSA
 KIMQLQQLVNMFADLQRRYGEKI
 HKLTLHGGFSCPNRDGTGRGGCTFCQVASFAD
 QMQQQSITQQLAIQAKKANRANRY
 LAYFQAYTSTYAEVNALAAMYQQALCEADIVGLC
 VGTRPDCVPDAVLDLLSSYQQQGY

gene 136757..141364

CDS 136757..141364

EVWLELGLQTANDKTLKRINRGHDFACYQQTARR
ARARGLKVCCHLIVGLPGEDRAQG
RETLEKVVTTGVDGIKLHPLHIVEGSTMAKAWRA
GRLTALALEDYVLTAGEMIRHTPA
EVVYHRISASARRPTLLAPLWCENRWTGMNELNN
YLLQHGVQGTAGDAYCYR"
/gene="gltB"
/locus-tag="y0128"
/gene="gltB"
/locus-tag="y0128"
/function="enzyme; central
intermediary metabolism: Pool,
multipurpose conversions"
/note="residues 43 to 1535 of 1535
are 87.55 pct identical to
residues 24 to 1517 of 1517 from
E. coli K12 : B3212; residues 51
to 1535 of 1535 are 89.23 pct
identical to residues 1 to 1486 of
1486 from GenPept :
>gb|AAK94787.1| (AY035435)
glutamate synthase large subunit
[Klebsiella aerogenes]"
/codon-start=1
/transl-table=11
/product="glutamate synthase,
large subunit"
/protein-id="AAM83722.1"
/db-xref="GI:21956794"
/translation="MRTITRGHWRAEKQICRKA
RVCQPTLSDINMSFTSWFVRVSQS
LGRFTDMLYDQSQERDNCGFLIAHIEGEP SHKV
VRTAIHALARMQHRGAILADGKTG
DGCGLLLQKPDHFFRMVAEERGWRLAKNYAVGMM
FLSQDEELAKASRRIVEEELQNET
LSIVGWREVPTNPDVLGEIALSSLPRIEQIFVNA
PAGWRSRDMERRLFVARRRIEKRI
SDKDFYACSFNLVTIYKGLCMPADLPRFYDLA
DLRLESAICLFHQRFSTNTVPRWP
LAQPFYLAHNGEINTIAGNRQWAKARAYKFKTP
LIPDLQDAAPFVNETGSDSSSLDN
MLELFLSGGMDLIRAMRLVPPAWQNNPDMDTD
RAFFDFNSMHMEPWDPAGIVMSD
GRYAACNLDRNGLRPARYVITKDKLITCASEVGI
WDYQPDEVVEKGRVGP GELMVIDT
RSGKILHSAETDNDLKSHPYKEWMEKNVKRLVP
FEDLPEEQVGSRQLDDSQLETYQK
QFGYSNEELDQIIIRVLGENGQEATGSMGDDTPFA
VLSSGPRIIYDYFRQQFAQVTNPP
IDPLREAHVMSLATSIGREMNVFCEAEGQAHRLS
FKSPILLYSDFQQLTTLEGEHYRA
DRLDLTFNPAENDLEQAVLSLCDEAERKVRDGAV
MLVLSDRAIAPNRLPVPAPMAVGA
IQTRLVDKSLRCDANIIVETASARDPHHFAVLLG
FGATAIYPYLAYESLAKLVDSQAI
DKKYRDVMLNRYNGINKGLYKIMSKMGISTVAS
Y
RCAKLFEAVGLHRDLSDLCFQGVV
SRIGGASFSDFQQDLQNL SKRAWLKRKPLDQGG
L
LKFBVHNGEYHAYNPVSTLQKAV
HSGEYSDYQAYAKLVNERPIATLRDLLAIKPQGT
PIPVDQVEPAESLFKRFDTAAMSI
GALSPEAHESLAIAMNSLGGFSNSGEGGEDPARY

		GTNKVSRIKQVASGRFGVTPAYLV NADVIQIKVAQGAKEGGQLPGDKVTPYIAKLR YSVPGVTLISPPPHHDIYSIEDLA QLIFDLKQVNPAMISVKLVSEPGVGTIATGVAK AYADLITIAGYDGGTGASPLSSVK YAGCPWELGLVETQQALVANGLRHKIRLQVDGGL KTGVDIVKAAILGAESFGFGTGPM VALGCKYLRLCHLNNCATGVATQDEKLRRDHYHG LPERVVNYFHFIARETREIMAEELG VSQLVLDLIGRTDMLLELDGISAKQNKLDLSPMLK TATPHPGKALYCTESNPPFDKGLL NKELLSQAEPYIEAKQSKTFYFDIRNTDRSVGAA LSGAIATKHGDQGLATDPIKAYFS GTAGQSFGVWNAGGVELMLTGDANDYVGKGMAGG RIAVRPPVGSNFRSHEASIIIGNTC LYGATGGKLFAGRAGERFAVRNSGAIIVVEGIG DNGCEYMTGGIVCVLGRGTGINFGA GMTGGFAYVLDEDEGEFRKRVNPELV EVL DVEQLAIHEEHLRGLITEHVQLTGSSRGEE ILANWPEWVTKFALVKPKSSDVKALLGHRSRSA ELRVQAQ"
gene	141374..142792	/gene="gltD"
CDS	141374..142792	/locus-tag="y0129" /gene="gltD" /locus-tag="y0129" /function="enzyme; central intermediary metabolism: Pool, multipurpose conversions" /note="residues 1 to 472 of 472 are 84.32 pct identical to residues 1 to 472 of 472 from E. coli K12 : B3213; residues 1 to 472 of 472 are 84.74 pct identical to residues 1 to 472 of 472 from GenPept : >gb AAK94788.1 (AY035435) glutamate synthase small subunit [Klebsiella aerogenes]" /codon-start=1 /transl-table=11 /product="glutamate synthase, small subunit" /protein-id="AAM83723.1" /db-xref="GI:21956795" /translation="MSQNVYQFIDLQRVDPPKKP LKIRKIEFVEIYEPFSETQAKAQA DRCLSCGNPYCEWKCPVHNYIPNWLKLANEGRIM EAADLAHQTNLSPEVCGRVCPQDR LCEGSCTLNDEFGAVTIGNIERYISDKAIAMGWK PDMSHVHPTGKRVAVIGAGPAGLA CADVLARNGVQAVVFDHRPEIGLLTFGIPAFKL EKEVMIKRRKIFSEMGIEFQLNTE VGKDIITMEALLKDYPDVFVLGVGTYSMRGGLENE EANGVYDALPFLIANTKQLMGYEA TAHEPYINMQGKRVVVLGGGDTAMDCVRSSIRQG ATDVVCAYRRDEVNMPGSKREVKN AREEGVEFKFNLQPLSIEVNSNGKVCVGRMVRTQ LGAPDAQGRRMAEQIPGSEHVLPA DAVVMAGFRPHSMEWLAHDKLDKQGRVIAPE STDNAFQTSNPKIFAGGDIVRGSD LVVTAIAEGRKAADGIMNYLEV" /locus-tag="y0130"
gene	143233..143718	

CDS	143233..143718	/locus-tag="y0130" /note="residues 22 to 72 of 161 are 33.33 pct identical to residues 2690 to 2740 of 3744 from GenPept : >gb AAB68923.1 (U00060) Tralp [Saccharomyces cerevisiae]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83724.1" /db-xref="GI:21956796" /translation="MKFHLPFIVGGLLAMSSSAF AMSLNYQEVGYNIEARGARAVVAE LEKSGQLPAVENNIKLGDDNWIAMAPKLASAGNP KFTEGVKSALSSALIYNPAAVLKA VSGSKILTSLSDVCTAPIDVKDSEAKANFQQRASR TLLTIKNSDMAGPRDSCLAELKKL S"
gene	complement(143871..144386)	/gene="sspB"
CDS	complement(143871..144386)	/locus-tag="y0131" /gene="sspB" /locus-tag="y0131" /function="regulator; global regulatory functions" /note="residues 1 to 171 of 171 are 72.51 pct identical to residues 1 to 165 of 165 from E. coli K12 : B3228" /codon-start=1 /transl-table=11 /product="stringent starvation protein B" /protein-id="AAM83725.1" /db-xref="GI:21956797" /translation="MEMSDMSPRRPYLLRAFYEW LIDNQLTPHLVVDVTRPGVSVPM FARDGQIVLNVAPRAVGNLELSNDDVRFNARFGG VPRQVTVPPIAAVMAIYARENGSGT MFEPEAAAYDADADGNFEGIEGKENETAPTESLML VTDDTRVEQDDDNSPDDKPPQPPR SGGRPALRVVK"
gene	complement(144392..145033)	/gene="sspA"
CDS	complement(144392..145033)	/locus-tag="y0132" /gene="sspA" /locus-tag="y0132" /function="regulator; global regulatory functions" /note="residues 1 to 209 of 213 are 83.73 pct identical to residues 1 to 209 of 212 from E. coli K12 : B3229; residues 1 to 213 of 213 are 100.00 pct identical to residues 1 to 213 of 213 from GenPept : >emb CAC92790.1 (AJ414157) putative stringent starvation protein A [Yersinia pestis]" /codon-start=1 /transl-table=11

		<pre> /product="regulator of transcription; stringent starvation protein A" /protein-id="AAM83726.1" /db-xref="GI:21956798" /translation="MAVAANKRSVMTLFSGPTDI FSHQVRIVLAEKGVSVIEIEQVEAD NLPQDLIDLNPYRTVPTLVDRELTLYESRIIMEY LDERFPHPLMPVYPVARGSSRLM MHRIEHDWYSLLYKIEQGNAQEAEARKQLREEL LSIAPVFNETPFFMSEEFSLVDCY LAPLLWRLPVLGIEFTGAGSKELKGYMTRVFERD AFLASLTEAEREMHLKTRS" </pre>
gene	complement(145407..145805)	<pre> /gene="rpsI" </pre>
CDS	complement(145407..145805)	<pre> /locus-tag="y0133" /gene="rpsI" /locus-tag="y0133" /function="structural component; ribosomal proteins - synthesis, modification" /note="residues 3 to 132 of 132 are 92.30 pct identical to residues 1 to 130 of 130 from E. coli K12 : B3230; residues 3 to 132 of 132 are 93.07 pct identical to residues 1 to 130 of 130 from GenPept : >gb AAL22213.1 (AE008854) 30S ribosomal subunit protein S9 [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="30S ribosomal subunit protein S9" /protein-id="AAM83727.1" /db-xref="GI:21956800" /translation="MAMAENQYYGTGRKSSSAR VFLKPGSGKIVINQRSLEVYFGRE TARMVVNQPLELVDMMVKFDMYITVKGGGISGQA GAIRHGITRALMEYDESLRGELRK AGFVTRDAREVERKKVGLRKARRRPQFSKR" </pre>
gene	complement(145814..146257)	<pre> /gene="rplM" </pre>
CDS	complement(145814..146257)	<pre> /locus-tag="y0134" /gene="rplM" /locus-tag="y0134" /function="structural component; ribosomal proteins - synthesis, modification" /note="residues 6 to 147 of 147 are 95.07 pct identical to residues 1 to 142 of 142 from E. coli K12 : B3231" /codon-start=1 /transl-table=11 /product="50S ribosomal subunit protein L13" /protein-id="AAM83728.1" /db-xref="GI:21956801" </pre>

		/translation="MGKLLMKTFTAKPETVKRDW YVVDASGKTLGRLATELARRLRGK HKAEYTPHVDTGDIIVLNAEKVAVTGNKRTDKI YYHHTGFVGGIKQATFEEMIARRP ERVIEIAVKGMLPKGPLGRAMYRKLKVYAGTEHN HAAQQPQVLDI "
gene	complement(146556..147695)	/locus-tag="y0135"
CDS	complement(146556..147695)	/locus-tag="y0135"
		/note="residues 5 to 378 of 379 are 64.97 pct identical to residues 1 to 373 of 375 from E. coli K12 : B3232; residues 5 to 379 of 379 are 66.66 pct identical to residues 1 to 374 of 374 from GenPept : >gb AAL22215.1 (AE008854) putative ATPase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83729.1" /db-xref="GI:21956802" /translation="MRINMQQSSPITLYQQALDA GGYQPDDVQRRVARLETIYQALN QYQNVPAASASLRNRLGRLFGKPARPPVSPVQG LYMWGGVGRGKTWLMDLFFHSLPG ERKLRLHFHFRFMLRVHQELTELQGHENPLEIVAD GFKAQTDVLCFDEFFVSDITDAML LATLLEALFARGITLVATSNIPPDNLYHNGLQRG RFLPAIALIKQHCEVMNVDAIDY RLRTLQANLYLTPLNSQTEQAMAAIFVKLAGKE GGKATVLEVNRPLPAICVAEGVL AVDFHTLCEEARSQLDYIALSKRYHTVLLHNVRC MAARDENTARRFLALVDEFYERRV KLIIAAEASMFIEIYSGERLKFYQRCLSRQEMQ SEEYLSLPHLP "
gene	147907..148311	/locus-tag="y0136"
CDS	147907..148311	/locus-tag="y0136"
		/note="residues 1 to 127 of 134 are 80.31 pct identical to residues 3 to 128 of 134 from E. coli K12 : B3233; residues 1 to 127 of 134 are 80.31 pct identical to residues 3 to 128 of 134 from GenPept : >gb AAL22216.1 (AE008854) putative periplasmic protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83730.1" /db-xref="GI:21956803" /translation="MTWEYALIGLVGVVIGAVA MRFGNRKLRRQQVLQNELEKSKTD LEEYRQELVGHFARSAELLDNMARDYRQLYQHMA KSSNNLLPDLPLQDNPFYRLTES EADNDQAPVKLPPRDYSEGASGLLRPEHQNRD "
gene	148564..149955	/gene="degQ" /locus-tag="y0137"

CDS	148564..149955	/gene="degQ" /locus-tag="y0137" /function="enzyme; degradation of proteins, peptides, glyco" /note="residues 7 to 463 of 463 are 72.05 pct identical to residues 1 to 455 of 455 from E. coli K12 : B3234; residues 7 to 463 of 463 are 72.92 pct identical to residues 1 to 455 of 455 from GenPept : >gb AAL22217.1 (AE008854) serine endoprotease [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="serine endoprotease" /protein-id="AAM83731.1" /db-xref="GI:21956804" /translation="MREFKSMKKTSLLLSALAIS VGLGLASVPMVSAAALPAAVAGQT LPSLAPMLEKVLPAVSVHVSGSQAQQQRLPEEF KFFFGPNAPSGKESSRPFEGLGSG VIINAEGGYILTNNHVINNADKIRVQLNDGREYD AKLLGRDEQTDIALQLTDAKNLT AIKIADSDNLRVGDFAVAVGNPFGLGQTATSGII SALGRSGLNLEGFENFIQTDASIN RGNSSGALVNLDGELIGINTAILAPGGGNIGIGF AIPSNMAQNLSQQLIEFGEVKRGL LGIRGSEMTADIAKAFNIDAQRGAFVSEVLPKSA AAKAGIKPGDVLISVDGKKISSFA ELRAKVGTTGPGKTIKIGLLREGKPLEVSVTLDN SSSTSTSAENLSPSLQGASLSNGE LKDGSKGIVDSVTKGSPAAQSGLQKDDVIIAVN RERVKDIAELRKAIEAKPAVIALN IVRGEDNIYLLIR" /note="insertion element"
repeat-region	complement(149966..150675)	/insertion-seq="IS1541a"
gene	complement(150072..150581)	/locus-tag="y0138"
CDS	complement(150072..150581)	/locus-tag="y0138" /function="IS and transposon related functions" /note="IS1541a; residues 1 to 169 of 169 are 99.40 pct identical to residues 1 to 169 of 169 from GenPept : >gb AAC82673.1 (AF074611) transposase [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83732.1" /db-xref="GI:21956805" /translation="MRSGNCKCSTRNQKGVPMRD EKSLAHTRWNCKYHIVFAPKYRRQ VFYREKRRRAIGSILRKLCEWKNVNILEAECCVDH IHMLLEIPPKMSVSGFMGYLKGKS SLMLYEQFGDLKFKYRNREFWCRGYVVDIVGKNT ARIQEYIKHQLEEDKMGEQLSIPY PGSPFTGRK"

gene	150756..151844	/gene="degS"
		/locus-tag="y0139"
CDS	150756..151844	/gene="degS"
		/locus-tag="y0139"
		/function="enzyme; degradation of proteins, peptides, glyco"
		/note="residues 1 to 349 of 362 are 71.22 pct identical to residues 1 to 350 of 355 from E. coli K12 : B3235"
		/codon-start=1
		/transl-table=11
		/product="protease"
		/protein-id="AAM83733.1"
		/db-xref="GI:21956806"
		/translation="MFLKLLRSIILGLIVAGILL VALPMLRSPGYLFSGKSNNVNEEV PTSYNQAVRRRAAPAVNVNRSLSATQQGLAIRT LGSGVIMSDKGYILTNNKHVINDAE QIIIVAMQNGRISEALLVGSDNLTDLAVLKIDATN LPVIPININRTPHIGDVVLAIGNP YNLGQTVTQGIISATGRIGLSSSGRQNFLQTDAS INQGNSSGALVNTLGELMGINTLS FDKSNNGETPEGIGFAIPTALATKVMEKLIRDGR VIRGYIGITGEEYPPFNANDNGSD RVHGIKVKKVSPDGPAAQAGIHVGDIILNVNNKP ATSVIETMDQVAEVRPGTTIPVLL LRNGQQIAVQITITELDQNEMLTTQAAD"
gene	complement(152025..1532 87)	/gene="murA"
		/locus-tag="y0140"
CDS	complement(152025..1532 87)	/gene="murA"
		/locus-tag="y0140"
		/function="enzyme; murein sacculus, peptidoglycan"
		/note="first step in murein biosynthesis; residues 1 to 420 of 420 are 88.80 pct identical to residues 1 to 419 of 419 from E. coli K12 : B3189; residues 1 to 420 of 420 are 100.00 pct identical to residues 1 to 420 of 420 from GenPept : >emb CAC92798.1 (AJ414157) UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Yersinia pestis]"
		/codon-start=1
		/transl-table=11
		/product="UDP-N-glucosamine 1-carboxyvinyltransferase"
		/protein-id="AAM83734.1"
		/db-xref="GI:21956807"
		/translation="MDKFRVQGRTRLSGEVTISG AKNAALPILFAALLAEEPVELQNV PKLKDIDTTIKLLSQLGTKIERNNGSVFVDASAV NEFCAPYDLVKTMRASIWALGPLV ARFGQQQVSLPGGCAIGARPVDLHITGLEQLGAE IKLEEGYVKASVNGRLKGAHIVMD KVSVGATVTIMSAATLAEGTTVIENAAREPEIVD TANFLNTLGAKISGAGTDTRITIEG"

```

VTRLGGGVYRVLPDRIETGTFLVAAAISSGKVVV
RQTRPDTLDAVLAKLREAGADIEV
GDDWISLDMQGKRPKAITFRTAPHPGFPTDMAQ
FSLNLVAEGTGVITETIFENRFM
HVP ELIRMGAAEIESNTVICYGVEQLSGAQVMA
TDLRASASLVLAGCIAEGVTIVDR
IYHIDRGYERIEDKLRALGAKIERVKGE"
gene      complement(153441..1537 /locus-tag="y0141"
04)
CDS       complement(153441..1537 /locus-tag="y0141"
04)
          /note="residues 4 to 87 of 87 are
          80.95 pct identical to residues 6
          to 89 of 89 from E. coli K12 :
          B3190; residues 4 to 87 of 87 are
          80.95 pct identical to residues 6
          to 89 of 89 from GenPept :
          >gb|AAG58324.1|AE005547-10
          (AE005547) orf, hypothetical
          protein [Escherichia coli O157:H7
          EDL933]"
          /codon-start=1
          /transl-table=11
          /product="hypothetical protein"
          /protein-id="AAM83735.1"
          /db-xref="GI:21956808"
          /translation="MNLMDTNEIKDVL MNALALQ
          EAHVTGDGSHFQVIVVGELFADMN
          RVKKQQAVYAPLMEYIADNRIHALSIKAYTPQEW
          QDRKLNLF"
gene      complement(153842..1541 /locus-tag="y0142"
44)
CDS       complement(153842..1541 /locus-tag="y0142"
44)
          /note="residues 1 to 90 of 100 are
          43.33 pct identical to residues 33
          to 122 of 129 from E. coli K12 :
          B3191; residues 1 to 90 of 100 are
          43.33 pct identical to residues 33
          to 122 of 129 from GenPept :
          >gb|AAG58325.1|AE005547-11
          (AE005547) yrbB gene product
          [Escherichia coli O157:H7 EDL933]"
          /codon-start=1
          /transl-table=11
          /product="hypothetical protein"
          /protein-id="AAM83736.1"
          /db-xref="GI:21956809"
          /translation="MAGELSWQSLQETLVLQGEL
          DRETLLPLWQQRETLLADKSRIDV
          SQLQRVDSSGLALLVHFRELQSQRGHSLEIIGIS
          NRLATLIELYNLQQIIPVETAS"
gene      complement(154180..1548 /locus-tag="y0143"
03)
CDS       complement(154180..1548 /locus-tag="y0143"
03)
          /note="residues 1 to 207 of 207
          are 77.51 pct identical to
          residues 1 to 209 of 211 from E.
          coli K12 : B3192; residues 1 to
          207 of 207 are 77.51 pct identical
          to residues 1 to 209 of 211 from

```

```

GenPept : >gb|AAL22179.1|
(AE008852) putative ABC
superfamily (atp and memb),
transport protein [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83737.1"
/db-xref="GI:21956810"
/translation="MFKRLFMVALLAIAPLVHAV
DQSNPYRLMDEAAKKTFTRLKNEQ
PKIKQNP DYLR TIVRELLPFVQIKYAGALVLGS
YYKDATPAQREAYFNAFGKYLEQA
YGQALALYHGQTYDVAPDQPLGDANIVAIRVTIL
DPSGRPPVRLDFQWRKNSQTGNWQ
AYDMIAEGVSMISTKQNEWASILRQKGV DGLTQQ
LLSAAKQPITL DK"
gene      complement(154816..1553 /locus-tag="y0144"
88)
CDS       complement(154816..1553 /locus-tag="y0144"
88)

/note="residues 6 to 178 of 190
are 71.67 pct identical to
residues 1 to 170 of 183 from E.
coli K12 : B3193; residues 6 to
184 of 190 are 67.59 pct identical
to residues 1 to 179 of 183 from
GenPept : >gb|AAL22180.1|
(AE008852) putative ABC
superfamily (bind-prot) transport
protein [Salmonella typhimurium
LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83738.1"
/db-xref="GI:21956811"
/translation="MGTESMQTKKSEVVWGMFIL
IAILAVIFLCLKVADIKSVGNQPT
YRIYANFDNIGGLKNHSPVKIGGVVGRVAEITL
DTKNYTPRVAIDIQQRYNHIPDTS
SLAVRTSGLLGEQFLALNVGFEDPEMGTSILKDG
GTIQDTSALVLEDLIGQFLYKSS
GDSPAVSETAPATETAAPQAAVPSLPAQHP"
gene      complement(155378..1561 /locus-tag="y0145"
60)
CDS       complement(155378..1561 /locus-tag="y0145"
60)

/note="residues 1 to 260 of 260
are 82.69 pct identical to
residues 1 to 260 of 260 from E.
coli K12 : B3194"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83739.1"
/db-xref="GI:21956812"
/translation="MLVKSLASLGRRGINVCASF
GRAGLMLFNALVGRPEPRKQWPLL
IKQLYSVGVSLLIIVVSGLFIGMVLGLQGFLIL
TTYSAEASLGMMVSLSLRELGPV

```

		VTALLFAGRAGSALTAEIGLMKATEQISSLEMM IDPLRRVVAPRFWAGLISMPLLTA IFVAVGIWGGSVVGVDWKIDSGFFWSAMQNAVE WRTDLLNCLIKSLVFALVTWIAL FNGYDAVPTSEGISRATTTRTVVHSSLAVLGLDFV LTALMFGN"
gene	complement(156378..1571 96)	/locus-tag="y0146"
CDS	complement(156378..1571 96)	/locus-tag="y0146" /function="putative transport" /note="residues 4 to 269 of 272 are 78.19 pct identical to residues 1 to 266 of 269 from E. coli K12 : B3195" /codon-start=1 /transl-table=11 /product="putative ATP-binding component of ABC transport system" /protein-id="AAM83740.1" /db-xref="GI:21956814" /translation="MKQLASNVNMLIEIRGMSFT RGERLIFADINMTVPRGKVTAIMG PSGIGKTTLLRLIGGQLAPDTGEIWFDDGNIPAL SRQRLYDVRKKMSMLFQSGALFTD LTVFENVAFPLREHSRLPEELLHSTVMMKLEAVG LRGAANLMPAELSGGMARRAALAR AIALDPELIMFDEPFVQDPITMGVLVKLIDELN HALGVTCVVVSHDVPEVLSIADYA YIVADQHVIAEGTPEQLQTNSDMRVRQFLDGIAD GPVPFRFPAGDYKTELLYPK"
gene	157461..158435	/locus-tag="y0147"
CDS	157461..158435	/locus-tag="y0147" /note="residues 1 to 318 of 324 are 60.69 pct identical to residues 1 to 318 of 325 from E. coli K12 : B3196; residues 1 to 318 of 324 are 63.52 pct identical to residues 1 to 318 of 325 from GenPept : >emb CAD07831.1 (AL627278) putative membrane protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83741.1" /db-xref="GI:21956815" /translation="MFLAITLLIIGLVLLVYGAD RLVYGA AVLRSRSGVPPLIIGMTI VGIGTSLPELIVSVTAALNGQTDMAVGNVLGSNI TNLLLIVGGAALIRPLIVRSEILR RELPLMLVVTALCGFLLADNHL SRGDGVILLAA AAFIVLMLKIARLAHAEGNDILTR EQLSELPQDSSTTVALLWLVLAFIILPLSAKMII DNATVIARVAGVSELVIGLTVIAI GTSLPELATFIAGALKGENDIAVGNIIIGSNIFNI VIVLGVPALLSPGEINPEAFQRDY WVMLAVSVVFTLLCLGRKHRIGHLAGALLLCGFI TYLAVLFFAPISAL"
gene	158459..159532	/locus-tag="y0149"
CDS	158459..159532	/locus-tag="y0149"


```

/feature "note" (30..357) {
    /note="residues 30 to 357 of 357
are 77.43 pct identical to
residues 1 to 328 of 328 from E.
coli K12 : B3197; residues 30 to
357 of 357 are 78.65 pct identical
to residues 1 to 328 of 328 from
GenPept : >gb|AAL22184.1|
(AE008852) putative polysialic
acid capsule expression protein
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="putative isomerase"
/protein-id="AAM83742.1"
/db-xref="GI:21956816"
/translation="MLRKAWSESNQHTYSVKDDG
NTNIGRILSMSTFDLQPGVDFQQA
GKQVLQIEREGLAQLDQYINEDFSRACEAIFRCH
GKVVMGMGKSGHIGCKIAATFAS
TGTPAFFVHPGEASHGDLGMITPQDIVLAISNSG
ESNEILTLPVLKRQKILLICMSS
NPESTMGKAADIHLCINVPQEACPLGLAPTTSTT
ATLVMGDALAVALLKARGFTQEDF
ALSHPGGALGRKLLLRISDIMHTGTEIPTVSPDA
SLRDALLEITRKSLGLTVICDDSM
RIKGIFTDGLRRVFDMGIDLNNAKIADVMTTRGG
IRVPPNILAVDALNLMESRHITAL
LVADGDQLLGVVHMDMLRAGVV"
}

gene      complement(159121..159408)
CDS       complement(159121..159408)

/feature "note" (18..78) {
    /note="residues 18 to 78 of 95 are
32.78 pct identical to residues
645 to 704 of 918 from GenPept :
>gb|AAA33114.1| (M33154) nitrate
reductase [Cucurbita maxima]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83743.1"
/db-xref="GI:21956817"
/translation="MFGGTRIPPRVMTSAIFALF
RSMPISNTRKSPSVKIPLILIES
SQITVKPRLFRVISSKASRNDASGLTVGISVPVC
IISLIRSSNLRPSAPPG"
}

gene      159781..160344
CDS       159781..160344

/feature "note" (5..187) {
    /note="residues 5 to 187 of 187
are 77.04 pct identical to
residues 6 to 188 of 188 from E.
coli K12 : B3198"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83744.1"
/db-xref="GI:21956818"
/translation="MSNTAYIDTCYGPVADDVIQ
RAANIRLLICDVGVMSDGLIYMG
NQGEELKAFNVRDGYGIRCLITSDIDVAIITGR
AKLLED RANTLGITHLYQGQSDKL
VAYHELLATLQCQPEQVAYIGDDLIDWPVMAQVG

```

gene	160341..160904	LSVAVADAHPLLLPKAHYVTRIKG
CDS	160341..160904	GRGAVREVCDLILLAQDKLEGATGLSI"
		/locus-tag="y0151"
		/locus-tag="y0151"
		/note="residues 1 to 186 of 187
		are 55.91 pct identical to
		residues 1 to 185 of 191 from E.
		coli K12 : B3199"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83745.1"
		/db-xref="GI:21956819"
		/translation="MSKTRRWITLVLALIALALI
		GWNMSGFNQQGAPVVADDNEPSSQ
		SQHTVTTVFNPVQQLNYKLVAEEVQNFSAKELTW
		FTKPVMTLFGDNAVATWTVRADRA
		KLTDDKMPLYLYGHVEVDSLTAQAQLKKIRTDNAQ
		VNLITQDVASDDEVTLFGIGFTSE
		GMRIRGNLRDKTAELIEKVKTSYEIQK"
gene	160867..161433	/locus-tag="y0152"
CDS	160867..161433	/locus-tag="y0152"
		/note="residues 8 to 177 of 188
		are 69.76 pct identical to
		residues 1 to 172 of 185 from E.
		coli K12 : B3200; residues 8 to
		187 of 188 are 69.94 pct identical
		to residues 1 to 183 of 184 from
		GenPept : >gb AAL22187.1
		(AE008852) putative ABC
		superfamily (bind-prot) transport
		protein [Salmonella typhimurium
		LT2]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83746.1"
		/db-xref="GI:21956820"
		/translation="MKRLKPLMKSKNKISHLLLA
		CSSLAASLSAFALTGDTEQPAEVK
		SDKQTLDMETNTVTFIDNVVIKQGTIEIKADKVV
		VTRPGGDQSKMIIIEGFGNPVTFYQ
		MQDSGKPVKGHGQKLRYEIANDFVVLTGDAYLEQ
		LDSNIKGDRITYLVKKQQMEAFSD
		KGKRVTTVLLPSQLQDKGPAASGQKKSK"
gene	161440..162165	/locus-tag="y0153"
CDS	161440..162165	/locus-tag="y0153"
		/function="putative transport"
		/note="residues 1 to 241 of 241
		are 88.79 pct identical to
		residues 1 to 241 of 241 from E.
		coli K12 : B3201; residues 1 to
		241 of 241 are 88.79 pct identical
		to residues 1 to 241 of 241 from
		GenPept : >gb AAL22188.1
		(AE008852) putative ABC
		superfamily (atp-bind) transport
		protein [Salmonella typhimurium
		LT2]"
		/codon-start=1
		/transl-table=11
		/product="putative ATP-binding

		component of ABC transport system"
		/protein-id="AAM83747.1"
		/db-xref="GI:21956821"
		/translation="MATLIAEKLAKAYKGRKVVE DVSLNVKSGEIVGLLGPNAGKTT TFYMVVGIVQRDAGRIVIDDEDISLLPLHERARR GIGYLPQEASIFRRLSVFNNLMAV LEIRKDLSAEQREERAEEELMEEFHINHLRDSLGO SLSGGERRRVEIARALANPKFIL LDEPFAGVDPISVIDIKKIIKHLRDSGLGVLITD HNVRETLDVCERAYIVSQGHLIAH GTPQDILADEQVKRVYLGEEFRL"
gene	162227..163660	/gene="rpoN"
		/locus-tag="y0154"
CDS	162227..163660	/gene="rpoN"
		/locus-tag="y0154"
		/function="regulator; global regulatory functions"
		/note="nitrogen and fermentation regulation; residues 1 to 477 of 477 are 82.59 pct identical to residues 1 to 477 of 477 from E. coli K12 : B3202; residues 1 to 477 of 477 are 82.38 pct identical to residues 1 to 477 of 477 from GenPept : >emb CAA26925.1 (X03147) ntrA protein (aa 1-477) [Klebsiella pneumoniae]"
		/codon-start=1
		/transl-table=11
		/product="RNA polymerase, sigma(54 or 60) factor"
		/protein-id="AAM83748.1"
		/db-xref="GI:21956822"
		/translation="MKQGLQLKFSQQLAMTPQLQ QAIRLLQLSTLELQQEIQLALESN PLLEQTDLHEEIDAKETVDSESLDTREALEQKDM PEELPLDATWDEIYTAGTPSGMGN DYSDDLPVYQGETTQTLQDYLWQVDLTPFTET DAAIATSIVDAVDDTGyltVPLED ILESMDENVALDEVEAVLKRIQHFDPIGVAARN LRECLLVQLSQYAKDTPYLAEARL IVSEYLDLLGNHDFRMMIRLSRLKEDTLKEAIAL IQSLDPRPGQSINTGESEYVIPDV LVRKEKGIWTVELNADSIPRLKVNQQYAAMGNSV RNDSDGQFIRSNLQEAkWLIKSL SRNETLLKVARCIVEQQVEFFEKGAEFMKPMVLA DIAQAVDMHESTISRVTQKFLHS PRGIFELKYFFSSHVNTDSGGEASSTAIRALVKK LVAAENPAKPLSDSKLTLLCEQG IMVARRTVAKYRESLSIPPSNQRKQLV"
gene	163684..163791	/locus-tag="y0155"
CDS	163684..163791	/locus-tag="y0155"
		/function="putative regulator; global regulatory functions"
		/note="residues 1 to 35 of 35 are 94.28 pct identical to residues 1 to 35 of 95 from GenPept : >gb AAL22190.1 (AE008852) putative sigma N modulation factor [Salmonella typhimurium LT2]"
		/codon-start=1

		/transl-table=11 /product="putative sigma-54 modulation protein" /protein-id="AAM83749.1" /db-xref="GI:21956823" /translation="MQLNITGHHVEITEALREFV TTKFAKLEQYFDRIN" /locus-tag="y0156" /locus-tag="y0156" /function="putative regulator; global regulatory functions" /note="residues 1 to 57 of 57 are 73.68 pct identical to residues 39 to 95 of 95 from E. coli K12 : B3203; residues 1 to 57 of 57 are 77.19 pct identical to residues 39 to 95 of 95 from GenPept : >emb CAA34391.1 (X16335) ORF95 peptide (AA 1-95) [Klebsiella pneumoniae]" /codon-start=1 /transl-table=11 /product="probable sigma-54 modulation protein" /protein-id="AAM83750.1" /db-xref="GI:21956824" /translation="MVLSVEKVKQIAEATVHVNG GELHASSEQEDMYAAIDILVDKLA RQLNKHKDKLKQH"
gene	163798..163971	
CDS	163798..163971	
		/gene="ptsN" /locus-tag="y0157" /gene="ptsN" /locus-tag="y0157" /function="enzyme; transport of small molecules; amino acids, amines" /note="regulates N metabolism; residues 7 to 158 of 164 are 86.18 pct identical to residues 4 to 155 of 163 from E. coli K12 : B3204; residues 7 to 158 of 164 are 86.18 pct identical to residues 4 to 155 of 163 from GenPept : >gb AAG58338.1 AE005548-9 (AE005548) phosphotransferase system enzyme IIA, regulates N metabolism [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="phosphotransferase system enzyme IIA" /protein-id="AAM83751.1" /db-xref="GI:21956825" /translation="MKDEMTNDPALQLSSVLNIE STKSSVHCSSKKRALEIISLAAK QLNLP SQVVFDAVLT RERMGSTGIGSGIAIPHGK LEEDTLRAVGVFIRLEQPIAFDAI DNQPVDLLFALLVPADQCKTHLHTLSLVAKRLAD KTVCRRLRSAQSDDELYQIITELP PEIA"
gene	164077..164571	
CDS	164077..164571	
		/locus-tag="y0158" /locus-tag="y0158"
gene	164877..165731	
CDS	164877..165731	

		/note="residues 1 to 283 of 284 are 94.34 pct identical to residues 1 to 283 of 284 from E. coli K12 : B3205" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83752.1" /db-xref="GI:21956826" /translation="MVLMIIVSGRSGSGKSVALRA LEDMGFYCVDNLPVVLLPQLASTL ADRNISAASIDVRNMPESPEVFEHAMTQLPDSF SPQLFLDADRNTLIRRYSDTRRL HPLSAKNLSLESAIDEESDLLEPLRSRADLIIDT SEMSVHELAEMLRTRLLGKREREL TMVFESFGFKHGIPIDADYVFDVRFLPNPHWDPK LRPMTGLDKPVISFLDRHTEVHNF IYQTRSYLEQWLPMLETNNRSYLTVAIGCTGGKH RSVYVAEQLDADYFRARGKNVQSRH RTLEKRKQ"
gene	165728..166000	/gene="ptsO"
CDS	165728..166000	/locus-tag="y0159" /gene="ptsO" /locus-tag="y0159" /function="transport; transport of small molecules; Other" /note="nitrogen related, exchanges phosphate with Enzyme I, Hpr; residues 1 to 90 of 90 are 87.77 pct identical to residues 1 to 90 of 90 from E. coli K12 : B3206; residues 1 to 90 of 90 are 85.55 pct identical to residues 1 to 90 of 90 from GenPept : >gb AAL22193.1 (AE008853) NPr, phosphocarrier protein HPr-like NPr, nitrogen related, exchanges phosphate with Enzyme I [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="phosphocarrier protein HPr-like NPr" /protein-id="AAM83753.1" /db-xref="GI:21956827" /translation="MTVKQTVEIKNKLGMHARPA MKLFELVQSFDAEVMLRNDSGTEA EASSVIALMLDSAKGRQIEVEATGVDEIQALAA VIELFNSGFDED"
gene	complement(165896..166147)	/locus-tag="y0160"
CDS	complement(165896..166147)	/locus-tag="y0160" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83754.1" /db-xref="GI:21956828" /translation="MHVVQQNIGGFSSFPANCG ELYSRLISLQGVKIVFFVLSKRLP TLRAPLIFVKSRIKQLDNRCQCLNFINPGCFNLY LAAFG"
gene	166338..167273	/gene="pyrB"

CDS	166338..167273	<pre> /locus-tag="y0161" /gene="pyrB" /locus-tag="y0161" /function="enzyme; pyrimidine ribonucleotide biosynthesis" /note="residues 1 to 311 of 311 are 84.88 pct identical to residues 1 to 311 of 311 from E. coli K12 : B4245; residues 1 to 311 of 311 are 85.85 pct identical to residues 1 to 311 of 311 from GenPept : >gb AAL23279.1 (AE008909) aspartate carbamoyltransferase, catalytic subunit [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="aspartate carbamoyltransferase, catalytic subunit" /protein-id="AAM83755.1" /db-xref="GI:21956830" /translation="MANPLYHKHIISINDLSRDE LELVLRTAASLKKTPQPELLKHKV IASCFFEASTRTRLSFETSIHRLGASVVGFSDDS NTSLGKKGETLADTMSVISTYVDA IVMRHPQEGASRLAAQFSGNVPIVNAAGDGANQHP TQTLDDLFTIQETQGRLDNINIAM VGDLKYGRTVHSLTQALAKFNGNHFFFIAPDALA MPAYILQMLEEKEIEYSLHESLEE VVPELDILYMTRVQKERLDPSEYANVKAQFILRS SDLTGARDNLKVLHPLPRIDEITT DVDKTPYAYYFQQAGNGIFARQALLLVLNAELA L" </pre>
gene	167279..167749	<pre> /gene="pyrI" </pre>
CDS	167279..167749	<pre> /locus-tag="y0162" /gene="pyrI" /locus-tag="y0162" /function="enzyme; pyrimidine ribonucleotide biosynthesis" /note="residues 3 to 153 of 156 are 78.80 pct identical to residues 1 to 151 of 153 from E. coli K12 : B4244; residues 3 to 156 of 156 are 83.11 pct identical to residues 1 to 154 of 154 from GenPept : >gb AAA26565.1 (J05033) aspartate transcarbamoylase [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="aspartate carbamoyltransferase, regulatory subunit" /protein-id="AAM83756.1" /db-xref="GI:21956831" /translation="MMMTQDYKLQVEAIKCGTVI DHIPAQIGFKLLSLFKLTATDQRI TIGLNLPSKRSGRKDLIKIENTFLTEQQANQLAM YAPDATVNRIDNYEVVKKLTLSLP ERIDAVLTCPNSNCISHNEPVDSSFTVKAQRGEI </pre>

gene	167848..168273	SLKCKYCEKEFDHLTVLHAD"
CDS	167848..168273	/locus-tag="y0163" /locus-tag="y0163" /note="residues 11 to 141 of 141 are 83.20 pct identical to residues 11 to 141 of 141 from E. coli K12 : B4243; residues 14 to 141 of 141 are 85.93 pct identical to residues 1 to 128 of 128 from GenPept : >gb AAL23277.1 (AE008909) putative translation initiation inhibitor [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83757.1" /db-xref="GI:21956832" /translation="MISLSALRKSGVKMLRAIKT KLAPAAIGPYVQGVDLGSMIMTSG QIPIDPKTGLVADDIAAQARQSLNVKAIVEAAG LKVADIVKTTVFVKDLNDFSIVNA TYEAFSTEHSAPFPARSCVEVARLPKDVKIEIEA IAVRR"
gene	168572..169048	/locus-tag="y0164"
CDS	168572..169048	/locus-tag="y0164" /note="residues 62 to 143 of 158 are 31.70 pct identical to residues 1565 to 1640 of 3016 from GenPept : >dbj BAA17634.1 (D90907) ORF-ID:slr1403 integrin alpha- and beta4- subunit domain homolog [Synechocystis sp. PCC 6803]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83758.1" /db-xref="GI:21956833" /translation="MKLRTWLLIPIICSPFFWGS TAIAKNGVAIPLPKRVAVLSEGD LESASVGTYSVAIFKNDTFLDFIAGGVFSRDGSI FQDNGKPRVEFTDINGDGNKELIV SQLTAGSGNYLRVDAFSLGPDSINKVLSIQSDTK SDYISLLKELCEICLPIDAPPH"
gene	169282..170235	/gene="treR"
CDS	169282..170235	/locus-tag="y0165" /gene="treR" /locus-tag="y0165" /function="regulator; osmotic adaptation" /note="residues 1 to 316 of 317 are 62.02 pct identical to residues 1 to 314 of 315 from E. coli K12 : B4241; residues 1 to 316 of 317 are 62.02 pct identical to residues 1 to 314 of 315 from GenPept : >dbj BAB38641.1 (AP002568) repressor of treA,B,C [Escherichia coli O157:H7]" /codon-start=1 /transl-table=11

		/product="repressor of treA,B,C" /protein-id="AAM83759.1" /db-xref="GI:21956834" /translation="MQNRLTIKDIARMSGVGKST VSRVLNNEGSVSPQTRERVEAVIR QHGFTPSKSARAMRGQSDKVVGIIIVSRLDSPSEN QAVRTMLPLFYQQGYDPILMESQF DTTLVSEHLHLILQQRHVDGVILFGFSGLTAEMLA PWQEKMVVLAREYRGFSSVCYDDE GAIYLLMDKLRQAGHRHISYIGVQSSDATTGMRR YQAYLDYSQQHGLTPMVALGELSY QSGFQLAPQVITPQTSALVCASDTIAMGVSKYLQ QQEREQPPIQVCGIGNTPLLHFLF PDTLTIELGYGRAGVKAQQLLDQLSNSQPIQQI IIPGQLV"
gene	170610..172061	/gene="treB"
CDS	170610..172061	/locus-tag="y0166" /gene="treB" /locus-tag="y0166" /function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="trehalose specific; residues 13 to 483 of 483 are 80.46 pct identical to residues 2 to 472 of 473 from E. coli K12 : B4240; residues 13 to 483 of 483 are 80.89 pct identical to residues 2 to 472 of 473 from GenPept : >dbj BAB38640.1 (AP002568) trehalose specific PTS system enzyme II [Escherichia coli O157:H7]" /codon-start=1 /transl-table=11 /product="PTS system enzyme IIBC" /protein-id="AAM83760.1" /db-xref="GI:21956835" /translation="MRARNLYGKDDKMGKVKQQD IDQLIVLVGGRENIATVSHCITRL RFVLKDPSIASPKEIENLSMVKGCFTNAGQFQVV IGPEVDDYYKALIAKIGQSEVDKE QTKLAARQNMTWFERGISHFAEIFFPLLPALISG GLILGFRNVIGDIPMSEGKTLAQM YPAWQTIYDFLWLLGEAIFFFLPVAICWSTVKKM GGTPVLGIVLGITLVSPQLMNSYL LGQQLPDVWNFGWFTIEKVGYYQAQVIPSILAGLA LGWIETNLKRIIPAYLYLVVVPVV SLLLAFLAHTLIGPFGRMIGDGVAVGVKAVMTG SFAPVGAALFGFLYAPLVITGVHQ TTLAIDMQMVQSMGGTPVWPLIALSNIAQASAVL GIIIIISRKINEREISVPAAISAYL GVTEPAMYGINLKYRFPMLCAMIGSALAGLICGL TGVMANIGVGGPLPGILSIQPQFW GIYAVAMLVAIVVPLALTILVYKRKERRGELPV"
gene	172156..173823	/gene="treC"
CDS	172156..173823	/locus-tag="y0167" /gene="treC" /locus-tag="y0167" /function="enzyme; degradation of small molecules; Carbon compounds" /note="residues 7 to 553 of 555"


```

are 73.85 pct identical to
residues 7 to 549 of 551 from E.
coli K12 : B4239; residues 7 to
553 of 555 are 73.12 pct identical
to residues 6 to 548 of 550 from
GenPept : >emb|CAD06914.1|
(AL627283) trehalose-6-phosphate
hydrolase [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="trehalase 6-P hydrolase"
/protein-id="AAM83761.1"
/db-xref="GI:21956836"
/translation="MNNPIPWWQHGVIIYQIYPKS
FQDSTGNGYGDLAAGVAQRLDYLQK
LGVDAIWLTPVYVSPQVDNGYDVADYCAIDPAYG
TLDDFKRLVAGAHQRGIRIIMDMV
FNHTSTEHAWFKASQDRNSPYRQFYIWRDGDGGD
GSLPNNWRSKFGGHAWQWHAASGQ
YYLHLFAPEQADLNWEHQPVREDELKKVCEFWADL
GVDGLRLDVINLVSKQQDFPNLDL
GDGRRFYTDGPRIHEFLQELSRDVFQPRRLMTVG
EMSSTRLEHCQRYAALGGDELSMT
FNFHHLKVDYLNGEKWSLMPPNRVELKHIFNQWQ
QGMHNRANALFWCNHDQPRIVSR
FGHEGALRLPAAKMLAMVLHGMQGTPIYIYQGEEI
GMTNPNFTDITQYRDVESLNMFAE
LSVAGREPDELLAILAAKSRDNRTPMQWDSSDN
AGFSQGTPWIAPCSNIYHEINVNA
LADADSVFYAYQYLIARLKQYDIFTFGDYQDLCP
QHPDLWCYLRWQKQLLVVANLS
EEPQRWQPEGLTLDGNWQLLMSSYDQSAFQPQDM
ILRGYEGIIYVCE"
gene      174176..174586 /gene="rnk"
CDS      174176..174586 /locus-tag="y0168"
                        /gene="rnk"
                        /locus-tag="y0168"
                        /function="regulator; central
intermediary metabolism:
Nucleotide interconversions"
                        /note="residues 1 to 134 of 136
are 64.92 pct identical to
residues 1 to 134 of 136 from E.
coli K12 : B0610"
                        /codon-start=1
                        /transl-table=11
                        /product="regulator of nucleoside
diphosphate kinase"
                        /protein-id="AAM83762.1"
                        /db-xref="GI:21956837"
                        /translation="MTKPTITINELDAERLDALL
AQPAFAGSVVATALNEELDRAEIL
PPNEIPADVVTMNSRVRFDLNSQEEHIRTLYVP
ASLKDSNEQLSVMAPLGAALLGLH
VNDEISWKLPGGDETRITVLELLYQPESAGEYHR
"
gene      complement(174818..1752 /gene="cybC"
10)
CDS      complement(174818..1752 /locus-tag="y0169"
10)      /gene="cybC"

```

		<pre> /locus-tag="y0169" /function="enzyme; energy metabolism, carbon: Electron transport" /note="residues 31 to 130 of 130 are 57.99 pct identical to residues 1 to 100 of 100 from E. coli K12 : B4236; residues 3 to 130 of 130 are 52.34 pct identical to residues 1 to 128 of 128 from GenPept : >gb AAL23259.1 (AE008908) cytochrome b(562) [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="cytochrome b(562)" /protein-id="AAM83763.1" /db-xref="GI:21956838" /translation="MSMGKTLMALITAALLSTSS LVMAASVADDMETIAEHYGKVLKA DSTAVIKQDLQAMRVAAVDAQKGIPTKLKSKVED SPEMKDFRFGMDVLIGEIDGALAL ADQGKLDEAKQAAQDFKDTRNTYHKKYR" </pre>
gene	complement(175412..176056)	/locus-tag="y0170"
CDS	complement(175412..176056)	<pre> /locus-tag="y0170" /note="residues 25 to 134 of 214 are 23.21 pct identical to residues 51 to 159 of 320 from GenPept : >gb AAC06973.1 (AE000710) pyridoxal phosphate biosynthetic protein PdxA [Aquifex aeolicus]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83764.1" /db-xref="GI:21956839" /translation="MIMPVLIRGSSNMIVMPSTY SPATIAREFKVIHEFELSSMKYGV IFDKNVPKAAIIRMNTESFNGIPRHRIIAALDLV AKQELGENVISVQRFWQDSALFQV EGMVVEQGARGKGLATLLYEELVVKCGVILMSDN KQYEAGKALWQKIAQESDKLAVFI LDSDVGQFYPPYCGDRVPYNGKGIPEEKIWSLHPD TTKWGVVLVAENREKISQYC" </pre>
gene	complement(176305..177645)	/gene="pmbA"
CDS	complement(176305..177645)	<pre> /locus-tag="y0171" /gene="pmbA" /locus-tag="y0171" /function="phenotype; proteins - translation and modification" /note="maturation of antibiotic MccB17, see tld genes; residues 1 to 446 of 446 are 82.73 pct identical to residues 5 to 450 of 450 from E. coli K12 : B4235" /codon-start=1 /transl-table=11 </pre>

		/product="PmbA/TldD family protein" /protein-id="AAM83765.1" /db-xref="GI:21956841" /translation="MKVVTQVAEQRKTLQAVAQ ALELARVGSDAAEVAVSKTTGISV STRFGEVENVEFNSDGALGITVYHQQRKGSASTT DLNPDAVARTVQAALDIARYTSPD PYAGPADKSLLAFDAPDLDFHFGDLDAEQGILL AARAEQAALQADKRITNTEGGSFN SHYGIVFGNSHGMLQSYCSSRHSLSSSVIAEHN GDMERDYAYTIGRRMEDLATPEWV GEECARRTLRLSPRKLPTMQSPVLFAAEVATGL FGHVLSAISGGNIYRKSTFLLDHL GQQILPEWLTIEEHPHLLRGLASTPFDSEGVRTL QREIVKDGVLQTYLLTSYSARKLG LQSTGHAGGIHNNWRIAGQGQDFAGMLKQLDKGLV VTELMGQGVSTVTGDYSRGAAGFW VENGEIQYPVSEITIAGNLKMDLRNIVSVGSDIE TRSNIQCGSVLLPVMKIAGE" /locus-tag="y0172" /locus-tag="y0172" /function="phenotype; Not classified" /note="residues 3 to 183 of 184 are 78.02 pct identical to residues 1 to 182 of 183 from E. coli K12 : B4234" /codon-start=1 /transl-table=11 /product="putative alpha helix protein" /protein-id="AAM83766.1" /db-xref="GI:21956842" /translation="MTMNKQPEDWLDDVPENKND DDDEIIWVSKSEIKRDAEALKDLG TELVDLGKNALERIPLDEDLLAAIELAQKIKKEG RRRQLQLIGKMLRARDVEPIQTAL DKLKNRHNQQISLFHKLETLRDRLIAEGDEAIPT VLELYPDADRQQLRSLVRNAQKEQ AANKPPKSFRQIFSYLRELAEEKQ" /locus-tag="y0173" /locus-tag="y0173" /note="residues 6 to 87 of 93 are 53.01 pct identical to residues 6 to 88 of 90 from E. coli K12 : B3239" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83767.1" /db-xref="GI:21956843" /translation="MVKVVFDFNHIPDLPAFYRA FSQNFALSEDFGANLDALWDVVTG EIALPVEIEFVHFSTRHQRRFAAIVLLLEEAE LAGRLHFNVVDEHIV" /locus-tag="y0174" /locus-tag="y0174"
gene	177820..178374	
CDS	177820..178374	
gene	complement(178486..178767)	
CDS	complement(178486..178767)	
gene	complement(178772..179245)	
CDS	complement(178772..179245)	

```

/feature="enzyme; macromolecule
degradation: Degradation of RNA"
/feature="residues 1 to 156 of 157
are 47.43 pct identical to
residues 1 to 148 of 149 from
GenPept : >gb|AAA86441.1| (M14442)
barnase (RNase) precursor
[Bacillus amyloliquefaciens]"
/codon-start=1
/transl-table=11
/product="putative ribonuclease"
/protein-id="AAM83768.1"
/db-xref="GI:21956844"
/translation="MNKRLMAILGAVLLLIAGAW
QGIDGVTVRDIGSSAELERPALSA
SAATESLTQHQQVVKYLQTHHRLPDFYLTKKQAR
EQGWDAQKGNLCDVLPGKAIGGDR
FSNRERQLPDAKGRHWREADVNYRCGRGSDRLL
YSNDGLIYLTQDHYKHFIRME"
gene      complement(179440..1797 /locus-tag="y0175"
78)
CDS      complement(179440..1797 /locus-tag="y0175"
78)

/feature="residues 1 to 112 of 112
are 59.82 pct identical to
residues 374 to 485 of 486 from
GenPept : >gb|AAL44216.1|
(AE009270) succinate semialdehyde
dehydrogenase [Agrobacterium
tumefaciens str. C58 (U.
Washington)]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83769.1"
/db-xref="GI:21956845"
/translation="MIADANEQMKVASEETFGPL
AACFRFSTEAQVIRANNTPFGLA
AYFYTQNLQRVFRVSEALESGMIGVNECSVSTEL
APFGGVKESGLGREGSVLGLDEFM
EVKTLHLGNL"
gene      complement(179775..1809 /gene="gabD"
08)
CDS      complement(179775..1809 /gene="gabD"
08)

/locus-tag="y0176"
/feature="enzyme; central
intermediary metabolism: Pool,
multipurpose conversions"
/feature="NADP-dependent activity;
residues 23 to 366 of 377 are
56.06 pct identical to residues 15
to 360 of 482 from E. coli K12 :
B2661"
/codon-start=1
/transl-table=11
/product="succinate-semialdehyde
dehydrogenase"
/protein-id="AAM83770.1"
/db-xref="GI:21956846"
/translation="MPAQNPLQHQRQHDGIYHIG

```

YFVGGKWSQAQEQFDVYNPATGEL
VARVAKSGKQETEEAAIKAASEAFPWRKTPAKQR
AEILQRWYLLIMEHQQSLAELMVS
EQGKPLKEALVEVAYAASFIQWFSEQAKRANGEI
IPSAKEGARILATREPIGVVAIT
PWNFPLAMLTRKLGPALAAGCTGLIKPANNTPLS
AFALLALAEQAGVPAGVLNGVVGD
THAISDAIMASSDVRKISFTGSTNVGKTLMRNAA
ATMKRISMELGGNAPYIVFDDADL
EAAVAGAMACKFRNAGQVCVCVNRFYIQDAIYDE
FVNRLAAEVKKLKVGNGMDKDVNM
GPLINLAGLEKVEEHVKDALEKGGRLLAGGIAMR
WAVISSQR"

gene complement(181175..1831 /locus-tag="y0177"
30)

CDS complement(181175..1831 /locus-tag="y0177"
30)

/note="residues 9 to 650 of 651
are 64.64 pct identical to
residues 11 to 652 of 655 from E.
coli K12 : B3240; residues 9 to
650 of 651 are 64.79 pct identical
to residues 11 to 652 of 655 from
GenPept :
>gb|AAG58368.1|AE005551-11
(AE005551) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83771.1"
/db-xref="GI:21956847"
/translation="MTHPSFIRLRFAFKLSFAIV
AALFLGFHLQLETPRWSVLTAIV
SAGPAFAAGGEPFSGAIRHRGWLRIIGTFIGCIG
GLVIVLTIRAPVLTMLCCLWAG
ICTWISSLVRVENSYAFGLAGYTALIIIVTTGET
PLLTPQFAVERCSEIVLGIVCAVM
ADLLFSPRSIKQDIDRLVDKVLVDQYRLLQLCIG
PAEKSEIDRAWNELVKNTTSLNGM
RSYLMMESSRWQRCNRRLQVLHTESLALITQACE
TYLVMSNHPEVISAEKTMSEPA
QTPAEIHQQMKKLRFIAASHSEAIPHTISSWVG
AATRYLLLSKGIQTNSSINQVEED
ILAGDAPVKPISAEGHHAMINGLRTGIATAIGGL
FWLWTGWTSGAGCMVMIAVVTSLA
MRTPNPRMALDFLVGVIIALPIGALYFMFIIPS
TQQSMLLLCISLGVLAFIIGIEVQ
KRRLGSLGTLASTINIIVLSNPMIFNVRQFLDSA
LGQIVGCFVSLIVLLLIRDNAKDR
TGRDLLNRVYSAVSALTNNKTKRGENHLPALYQ
QLNQLLMMFPADIDKYRLALTLII
AHQRLNRTEIPVNAELSAFHKQIRSTAERVITVN
NDQKRRYYFARLLQELDQYQQKLV
DYQAADAVIRPVKRLTEMLRKYQSALI"

gene complement(183132..1840 /locus-tag="y0178"
67)

CDS complement(183132..1840 /locus-tag="y0178"
67)

/function="putative membrane"
/note="residues 1 to 311 of 311"

```

are 72.66 pct identical to
residues 1 to 310 of 310 from E.
coli K12 : B3241; residues 1 to
311 of 311 are 100.00 pct
identical to residues 1 to 311 of
311 from GenPept :
>emb|CAC93154.1| (AJ414158)
putative HlyD family secretion
protein [Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="putative membrane
protein"
/protein-id="AAM83772.1"
/db-xref="GI:21956848"
/translation="MSTFSLKIIRVGITVLVVVL
AVIAIFNVWAFYTESPWTRDAKFT
ADVVAIAPDVSGLLTEVPVKDNQLVQKGQILFVI
DQPRYQQALAEAEADVAYYQTLAA
EKQRESSRRHRLGIQALSQEEIDQASNVLQTVQH
QLAKAIAVRDLARLDLERTTVRAP
AEGWVTNLNVHAGEFINRGATAVALVKKDTFYIL
AYLEETKLEGVKPGYRAEITPLGS
NRILHGTVDISIAGVTNSSSSADSKGLATIDNNL
EWVRLAQRVPVKIHLDSQYLY
PAGTTATVVITGPNDRDPHQASPMTKLMHRLREF
G"
gene      complement(184075..1842 /locus-tag="y0179"
78)
CDS      complement(184075..1842 /locus-tag="y0179"
78)
          /note="residues 1 to 66 of 67 are
          81.81 pct identical to residues 24
          to 89 of 90 from E. coli K12 :
          B3242"
          /codon-start=1
          /transl-table=11
          /product="hypothetical protein"
          /protein-id="AAM83773.1"
          /db-xref="GI:21956849"
          /translation="MSLLPVMVIFGLSFPPIFLE
          LLISLALFFVVRILQPTGIYEFV
          WHPALFNTALYCCLFYLTSLRFS"
gene      184581..185492 /locus-tag="y0180"
CDS      184581..185492 /locus-tag="y0180"
          /function="putative regulator"
          /note="residues 1 to 301 of 303
          are 80.73 pct identical to
          residues 1 to 301 of 309 from E.
          coli K12 : B3243"
          /codon-start=1
          /transl-table=11
          /product="putative transcriptional
          regulator LYSR-type"
          /protein-id="AAM83774.1"
          /db-xref="GI:21956850"
          /translation="MERLKQMSVFAKVVECGSFT
          AAARRLENSVSSISQTVSKLENEL
          NVKLLNRSTRRIGLTEAGRIYYQGCRMLQEVQQ
          VHEQLYAFNNTPTGTLRIGCSSTM
          AQNVLATMTADMLKAYPGLSVNLVAGIPAPDLIA
          DGLDVVIRVGALQNSGLFSRRLGA

```

gene	185744..186619	MPMVVCAAKSYLSQYGTPAKPSDMANFSWLEYNV RPDSNFELIAPEGITTQISPQGRF VTNDSQTMIRWLKAGAGIAYTPLMWVIEEIKRGE VEILFKHYHSDPRPVYALYTEKDK MPLKVQVCIDYLTEYFKRVADVQDYR"
CDS	185744..186619	/locus-tag="y0181" /locus-tag="y0181" /function="regulator" /note="residues 4 to 182 of 291 are 26.76 pct identical to residues 8 to 200 of 303 from GenPept : >gb AAC75958.1 (AE000375) putative transcriptional regulator LYSR-type [Escherichia coli K12]" /codon-start=1 /transl-table=11 /product="putative transcriptional regulator" /protein-id="AAM83775.1" /db-xref="GI:21956851" /translation="MVHMFISKNLLVFFTTVQEG SLTNAAVKLFTTPPPMSRSLKILE EELGFKLFTRTTSGCLKLTLEGAIFYQEIIYPTYVR LTEITKNYKKNKNGIINIATYQLN SDHAGVICDYFIKKGNFNIELRENIGDISQMDIV ISTKEIKGYDFDELTASCEIKLL YASHLNDLPDRVEYLKKLPFIQSSIFCSCCFKR FSHNLIQQGYSGNVLRIDDARVRH EIIKKGAGISLSTNYFFDKKISHSTEISFISDI NFDITYYIYFKSSVINKEFFIQYI TNNSLLQWQKAEKKH"
gene	complement (186780..186941)	/locus-tag="y0182"
CDS	complement (186780..186941)	/locus-tag="y0182" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83776.1" /db-xref="GI:21956853" /translation="MALFCFGLLMNRIISIRYNG CSMVDIILHNLPLYLGTAWDVKQ QVLTMCCLK"
gene	187032..189356	/gene="tcaA1" /locus-tag="y0183"
CDS	187032..189356	/gene="tcaA1" /locus-tag="y0183" /function="putative factor; extracellular functions; secreted proteins" /note="residues 182 to 557 of 774 are 35.41 pct identical to residues 602 to 996 of 1095 from GenPept : >gb AAL18449.1 (AF346497) toxin complex protein [Photorhabdus luminescens]" /codon-start=1 /transl-table=11 /product="putative toxin subunit" /protein-id="AAM83777.1" /db-xref="GI:21956854"

```

/translation="MQPEARTDLSLAEGIPERAN
EYADPASIQSLFSPGRYLCELYHV
AKELHEDGNKLHIDKRRPDLQELVLSNSNMNQEIV
SSLEILLNVLQTNAPLAKLAKDTE
AHANDVSFTLPYDDNLTVINAILEDKAISLREIA
ALLAENNDPWANPITPALVQEQLG
LNPASYALIDIKSPLDDNSAKRLAHATQLSVEQL
QWLNKNAIESSDKDSPLRPEILT
IISEYRRLHQRYGLSVDPFIAIINAVNTTHTNEN
KTSFFQQIFSTLDVDAGFNFLDQG
SWEVIIRKALGITAEELLRIAKYCFGKSSISNVK
MNSKKFSQLYRMAMIPRTLGVVSFS
QAEYLWQLYSHPDENIMEKIAQGNALTIIDAIIV
LENTLQWMSEQKLDITTLQAMLTk
QYSTTATPELFNFLSNIIYQTLGKQVYSESCLKPNL
YRSLANGFHLKANVVAGLVNWLAK
NDSEFTLERFWQNIISMTFAEEPSLHQLEIHQPLL
IQCQKLSQYVLIQAQWAEELSEQEIA
LILLPNGIDNRGSAPSPSITLLKLLSEFKLCQQE
AKVSQSELFDIMQQLITDTNEKQE
KLRNSADKVIRSIKSIKSGINNSMDDIDSTISIR
NGSATLFPPEHPMYKALKLEVSNI
EKSQIQLEGKKKEEIKLEQAKDNIQSLINNWD
EIIIRLADAYHWDINIANSIFILI
FGEKINFTFHYENRNDYHYEEHYGYRFEQKPMYS
FDKKLNGFGSILLKLNHIYIAEK
LKIHPGTIIKIKNYIFDDKSNELENIANKLRVNL
"

```

gene 189397..192990

CDS 189397..192990

```

/gene="tcbA"
/locus-tag="y0184"
/gene="tcbA"
/locus-tag="y0184"
/function="putative factor;
extracellular functions; secreted
proteins"
/note="residues 1 to 1196 of 1197
are 42.03 pct identical to
residues 1 to 1187 of 1189 from
GenPept : >gb|AAL18450.1|
(AF346497) toxin complex protein
[Photorhabdus luminescens]"
/codon-start=1
/transl-table=11
/product="putative toxin subunit"
/protein-id="AAM83778.1"
/db-xref="GI:21956855"
/translation="MPTSTVLNKNINESRRDALVN
YYLAKNVSGDEKIKTAEQLYQYLL
LDTKIGHEVKTSPIAEAISLQIYINRCVDGEEN
DLHEKNISTHFSNDFLHGWSYN
KRYARWAGKEKLMYYAADYIDPTLRYNKTELFNT
FEQSINNSRLTEKSVKSALQSYLI
SYEKLAQIDTIKELYVENIKTHFFLGKTRESPECQ
YYWRSGEQLSNDSHHLRWSEWKKV
NCNINGTEEKFFINLSWHRSSLYIDWINKFSIRT
DKDETTEKYHYNRVYKNDNTWSE
LIINMDIGFKLSTSTEVITLPPFFVNQGDPAKE
EVENLFLTNGTSIKRIESRLHGYI
NGHIKILCNDDGISFEIAEKLINGDNGTIGEVKI
IENEKIISTINNEKGENKKINLID
KFEIRIFPYNELVASTIVFNRIKPEEKIIDELDD
KISLLSPNSLPLKEKFQTSVDELL

```


gene

192987..197537

CDS

192987..197537

```
SYNTQKNNVKLNAFNGSYGIYWLWELFFHIPLLAS
MRFLNEQRFDLAQHWLKYLFNSAG
YRDGNGNLLKEGDNILYWNILPLQQDTAWDKNTL
IQATDDPDVIAMQDPMQYKLAIFM
RTLDLIISQGDQAYRQLERDTLAEAKIHYYIQASQ
LLGPRPNLNSSHQWENIKLAEESR
QLENSHFLPPYNELLLSYWDKLEIRLYNLRHNLN
LDGQPLHLPLFATPVDPKALQRQH
GAGNGINSSEQIATAQTSLYRFPLLIERAKSAVS
AVIQFGNSLQSVLERQDNEAMTLL
FQQQQQKVLQHTKDIQNNNIQVLQASLEATDSLK
SAAEQRRKHYKELLDNGISSDEQL
AINIRIASAALNGESLVPLGLSAVLDTAPNVFGL
ADGGSRWGAISQAVGWMQSMAMA
LETTAGVRDAKANYSRRAQEWTLQKDQADKDIEQ
LAHQYTSVQEQLNMAQKQLNLAEEL
EQGHADALYQMQRSTFTGKELYNWMAGRLSGLYF
QLFDATQPLCLMAKAALEKEVDKA
KTDGLFIRSGWNDLYQGLLAGEDLQLNLQKLENV
WLMEEQRALEVERTVSLAQHYQQQL
SDHKFNLAIEIVTGYMAQDKDQKTGNEQDFVELKN
GTLITSLSIKGLNLVEDYPETMHL
GDIRRIKQISVSLPALLGPYQDVQATLDYAGENT
HLAKGCTALAI SRGMNDSGQFLLD
FNDGKYL PFEGIDISDKGTLVLRFPNATSKQKLL
LQSLSDIILHIRYTIRS"
/gene="tcaC1"
/locus-tag="y0185"
/gene="tcaC1"
/locus-tag="y0185"
/function="putative factor;
extracellular functions; secreted
proteins"
/note="residues 21 to 1511 of 1516
are 48.90 pct identical to
residues 1 to 1473 of 1476 from
GenPept : >gb|AAL18487.1|
(AF346500) toxin complex protein
[Photorhabdus luminescens]"
/codon-start=1
/transl-table=11
/product="putative toxin subunit"
/protein-id="AAM83779.1"
/db-xref="GI:21956856"
/translation="MITPLPQSTGPTEGLIGEPF
MENSKQQVAVAPLSLPKGGGAITG
MGDSLGP IGP SGMATLTLPLPISAGRGYAPSLTL
SYSSGSGNGPFGLGWQLGTMAIRR
RTNAQVPRYDEYDEFLAPNGEVMVVAADPQGSIE
RTEQSLNGEQFSVIRYLPRIEGNF
HRIEYWRPRTNNSQAPFWLVHSSDGQKHCLGYSA
AARIADPLHPEHIAEWLLEESVSL
SGEHIGYQYQAEDEQGIDEPSIYKAEKQNHPAAS
AQRYLKRVVYGNRQAAYELYCLTQ
QPAPTSWLFSLIFDHGEYSNIAEQVPV I IKGKSW
NFRQDAF SHFN YGF EVRTRRLCQQ
VLMYHNLSALKGDEPDAQATLVSRRLRLHYQHDAY
ATQLVGCQQLAHEPDGTRKSLPPL
EFDYQDFSTRDALGWQPLTDWAEFNYQYQMVDLN
GEGMPGMLYQDSGHWIYRPPVRQP
GTADGITFGAAQRLPSLPAMRENAMLMDINGDGK
LDWVISQPGLAGYFSRDPDL SRDP
```

		DLSWTQFIPLSTLPAEYFHPQAQLVDLAGSGLSD LALVGPKSVRVYTNLCDSFAAATQ VAQDDITLPLPGVHFTLVAFSDVMGSGQQHLV RIRHNSVTCWPNLGHGRFGHPLSL PGFNQPVQFNPLAIYLADIDGSGTIDLIYATTS QLLIYRNQSGNRFAEPLAIALPTG IRFDNSCQLSLADIQGLGVASIMLSVPHPTTQHW RYDFVASKPYLLCTTNNNMGAESQ LLYRSSVQFWLDEKAQAAKQGRSLACQLPFPIHL LAQTTQFDEITGNSLSQTARYFHG FYDGVQREFSGFGRVDTLDTDTSAQGSAAERTAP TKSSRWFTGRAGNETLWQSEYWQ GDDQAYSLLPTRLTKEFINNTQGDELLSELDDNQ FWLHRALKGSLRSELYGLDDSEL ATQPYSVNSSRYQVRQIQSSADGISSPVALPMVL EQLSYHYERIAQDPQCSQQIVLRC NEYGHPLHSVTINYPRRDKARISPYSWLAKEHWD SHFDEQQQLRITESQQSYHHEIS DKFYVLGLPAGQRSVDLTYPDNFVPTAGIHWEEL QQPEGLLGTKAERTFTAQQQVFYT SDTIPGLVAYSQQAEDDQTLVALDELLPANERK QQLIKAGYQIAPRLFARTGETDIW VAQSGFTDYGDASRFYRPISQRSTQLVGKTILEW DATCCAVSDIILADYSITHAEYDY RFITPYLLIDINDNQHYIELDALGRVTSSRFAGT EIDPQTNKVIETGFPSIAEQPFSA PNSVDKALSLENT RIPVAQFSVYQPQSWMISLQL DDIEIWIRANNITPEYLFQNHILI DNYYLCPLALRRWGRQNNLLITEGVGLTLKNPMR QPPHILTVVDNYFSASEPQQHQQ TLAUSDGFGRVLLSARRVETGPSYSFDPENGLLV DDKGNLVQLEVDQRWAVSGRTEYD NKGLPRRRYQPYFFDNWIWLYIANN RTLKEAYADTHIYDPLGREIKVITAKGYLRTH YFPWFVISEDENDTASEITPNP"
gene	197671..197973	/locus-tag="y0186"
CDS	197671..197973	/locus-tag="y0186" /function="phage-and prophage-related functions" /note="residues 14 to 94 of 100 are 45.67 pct identical to residues 12 to 92 of 101 from GenPept : >gb AAG55972.1 AE005330-4 (AE005330) putative holin protein of prophage CP-933X [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="hypothetical phage protein" /protein-id="AAM83780.1" /db-xref="GI:21956858" /translation="MHVQVPIDFFITWVIIGTF SAWGGLVRYIVDQNNYEYEWVWG VLCQVIVSAFTGLIGSLFTLETGSSRYITFAIAG LFGAMGNTALKHLWQRFFFSK"
gene	197977..198387	/locus-tag="y0187"
CDS	197977..198387	/locus-tag="y0187" /function="phage-and prophage-related functions" /note="residues 13 to 136 of 136"

		are 57.36 pct identical to residues 5 to 132 of 213 from GenPept : >gb AAL41481.1 (AE009016) endolysin [Agrobacterium tumefaciens str. C58 (U. Washington)]" /codon-start=1 /transl-table=11 /product="hypothetical phage protein" /protein-id="AAM83781.1" /db-xref="GI:21956859" /translation="MDPMMNDKPTFRLSQISEHN LHHVHPDLVLIVRRALTLSHIDFR VIEGIRTPERQQRQMVNLNGHSKTMNSRHILTGHAVD LAPMVNNRIPWDDWHAFFVHVAKAM KQAAKAMELPLQWGGDWKNFRDGPHELPRECYP "
gene	198375..198743	/locus-tag="y0188"
CDS	198375..198743	/locus-tag="y0188" /note="residues 35 to 96 of 122 are 37.50 pct identical to residues 3 to 66 of 94 from GenPept : >gb AAK81976.1 AF303741-42 (AF303741) 042R [Chilo iridescent virus]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83782.1" /db-xref="GI:21956860" /translation="MLPMISLSTLFGLGKSMMLL AGVVAIVWGVQASRTLDRLNQENV QLTTQLARIGQINQQLTQHIQATTVQLKQAQEQE RLEREKSSSELQKRLRLAQKGNRCA EEPVPAAVIRMQQQSFSDBGK"
gene	198730..198903	/locus-tag="y0189"
CDS	198730..198903	/locus-tag="y0189" /note="residues 8 to 32 of 57 are 43.99 pct identical to residues 632 to 656 of 732 from GenPept : >dbj BAB15720.1 (AK024430) FLJ00019 protein [Homo sapiens]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83783.1" /db-xref="GI:21956861" /translation="MTVNECLPFPEVLLPPCQMP TFDVQTWGDYPHYVERTRLAMVRC NANRESALRFLQR"
gene	198944..201775	/gene="tccC1"
CDS	198944..201775	/locus-tag="y0190" /gene="tccC1" /locus-tag="y0190" /function="putative factor; extracellular functions; secreted proteins" /note="residues 13 to 699 of 943 are 53.30 pct identical to residues 12 to 694 of 760 from

gene

201800..204658

CDS

201800..204658

```
GenPept : >gb|AAL18492.1|
(AF346500) unknown [Photorhabdus
luminescens]"
/codon-start=1
/transl-table=11
/product="putative toxin subunit"
/protein-id="AAM83784.1"
/db-xref="GI:21956862"
/translation="MPNILPTDLCANTPTLAIHD
NRGFAIRTLAYNRRDHNETIGELI
SRNRYNASGQLIASRDPRLVDNFRYQYSLSGVP
LRTDSVDSGSTLQLADSAGRTVLT
LDAHHTRRWVEYETGEHSLGRPLSYHEQAKGGLK
TVTDRFFYATNSEQDKSGNLNGQC
VRHYDSAGLQALINQSIIGVPLQQQRLLTNPKG
PVDWFGKENWGARLSEQPFVSHS
TTDALGQLLTQTDAGHIIQRMAYNRAGQLIGSWL
TIKNSAEQVILRSLTYSAAGQKLR
EESGNGVITEYRYEPQTQRLIGIKTTTPAKKDRP
TRLQDLRYDYDPVGNILAIHNDAE
ATRFYRNQKIVPETTYRYDALYQLIEATGREADT
NGIQNSQLPALASLNSNQFVNYT
RSYHYDRAGNLLKIQHTGASQYSTHITVSDSSNH
GIQQQEGITARDIRSQFDAAGNQQ
QLQPGQPLRWNSRNQLQQVEPVPRNDGISDSESY
LYDGGGSRVVKTSLHKTHNAIQTR
SVIYLAGLELRSQYNGNNLTEDFQVITVGAAGRA
QVRVLHWERGQPVDIVNDQLRYSF
DNHLGSLALIELSDGDIISQEEYYPFGGTAVLAS
RNTVEAKYKTVRYSGKERDATGLY
YYGYRYYPWLGRWLSADPAGTIDGLNLYRMVRN
NPVGLMDGDGLMTDKLLAKHEANF
AKKNISSMAELKSEIEKLGLLPADSKQLFLHLNG
GESDDEPSGSSGSSGSSEILENTS
PHKIKNFHFISEINLATMPRPYKDFSSTEDMLE
SAERLKAYGSIDTLTLDLTSEDI
PEFTSILADKGINYIAEKQYEIIDYFSEDELSSE
NIDRIVNMIKTIQNNNHKVGIIHCA
AGNGRSGLIATAMIINKKYTQSRINSFEEKNKLK
EIIDKNKNEINVDAITYDAMKLVR
KTNPFAGERTTDIKAAREYSRYLYSKQNR"
/gene="tccC2"
/locus-tag="y0191"
/gene="tccC2"
/locus-tag="y0191"
/function="putative factor;
extracellular functions; secreted
proteins"
/note="residues 13 to 723 of 952
are 52.56 pct identical to
residues 12 to 716 of 760 from
GenPept : >gb|AAL18492.1|
(AF346500) unknown [Photorhabdus
luminescens]"
/codon-start=1
/transl-table=11
/product="putative toxin subunit"
/protein-id="AAM83785.1"
/db-xref="GI:21956863"
/translation="MSTSLPTQLCANTPALTIHD
NRGLAIRTLAYNRRDHNETVDELI
SRNRYNASGQLIASRDPRLVDNFRYQYSLSGVP
```

		LRTDSVDSGSTLQLADSAGRTVLT LDAHHTRRWVEYETGEHSLGRPLSYHEQAKGGLK TVTDRFFYATNSEQDKNCNLNGQC VRHYDSAGLQALISQSIIGVPLQQQRLLTNPKG PVDWFGEEKENWGARLSEQPFVSHS TTDALGQLLTQTDAGHIIQRMAYNRAGQLIGSWL TIKNSAEQVILRSLTYSAAGQKLR EESGNGVITEYRYEPQTQRLIGIKTTRPAKKDRP TRLQDLRYDYPVGNILAIHNDAAE ATRFYRNQKIVPETTYRYDALYQLIEATGREADT NGIQNSQLPALASLNSNQFVNYT RSYHYDRAGNLLKIQHTGASQYSTHITVSDSSNH GIQQQDGI IARDIRSQFDAAGNQQ QLQPGQPLRWNSRNQLQOVEPVPNRNDGISDSESY LYDGSGRRVAKISLHKTHNAIQTR SVIYLAGLELRGQHNDNNLTESFQVITVGAAGRA QVRVLHWESGQPVDIVNDQLRYSF DNHLGSALIELDSDGDIISQEEYYPFGGTAVLAS RNTVEAKYKTVRYSGKERDATGLY YYGYRYYQPWLGRWLSADPAGTIDGLNLYRMVRN NPIRWRDNNGLLTEEQINMYVNLF SNIGLKNDELKSELLKYGLSEEEQNQIYLNMLR PMQSGSSSSLSFPSESSSSSGST QSVDSGYLSPVRNYHFFEDIKLATMHRPYPKKQA SSDTITYSAEDLTEASPIKILIGL DLTSKNTQPYKSALAEKGIKYITKEKYEITDFFE EGGLSTEQIDLTVNKILKLQKKDL VGIHCGAGNGRSGVIASALSINKQYTTDKINSFD VTHSLRGSILKDTQTYQVDTVAK AVGIIREINPKAVERNQDVISLYRSHFLYTRKH TTSL"
gene	204594..204800	/locus-tag="y0192"
CDS	204594..204800	/locus-tag="y0192" /note="residues 1 to 65 of 68 are 27.69 pct identical to residues 146 to 210 of 237 from GenPept : >emb CAB73875.1 (AL139078) putative integral membrane protein [Campylobacter jejuni]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83786.1" /db-xref="GI:21956864" /translation="MLFPYIDILIFYIQENTLHH YNLLILNTFPILNREGVYTRNTDF LKSLILTAALAKIGLTNIPMLCWH"
gene	complement (204861..206306)	/gene="tldD"
CDS	complement (204861..206306)	/locus-tag="y0193" /gene="tldD" /locus-tag="y0193" /function="phenotype; Not classified" /note="suppresses inhibitory activity of CsrA; residues 1 to 481 of 481 are 84.40 pct identical to residues 1 to 481 of 481 from E. coli K12 : B3244; residues 1 to 481 of 481 are 84.61 pct identical to residues 1 to 481 of 481 from

```

GenPept : >gb|AAL22237.1|
(AE008855) suppresses inhibitory
activity of CsrA [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="PmbA/TldD family
protein"
/protein-id="AAM83787.1"
/db-xref="GI:21956865"
/translation="MSLSFVSEQLLTANKLNHQD
LFSVLGQLTERRLDYADLYFQSSY
HEAWVLEDSIIKDGSYNIDQGVGVRAVSGEKTGF
AYADQITLNALQQSAHAARSIVRD
TGNGKVHTLGEIAYQALYPLLDPLQSLSREDKIA
LLHRVDKVARAADKRVQEVASALT
GVYEQILVAATDGTLAADVRLVRLSVSVLVEDN
GKREERGACGGGGRFGYDYFLETVD
GEVRADNFANEAVRMALVNLSAIAAPAGAMPVVL
GAGWPGVLLHEAVGHGLEGDFNRR
GSSVFSGQMKGKLVASELCTVDDGTMQGRGSLA
IDDEGVPGQYNVLIENGILKGYMQ
DKLNARLMGVAPTGNRRRESYAHLPMPRMTNTYM
LAGQSTPEDIIASVEYGLYAPNFG
GGQVDITSGKFVSTSEAYLIEKGKITHAVKGAT
LIGSGIEAMQQISMVGNLALDKG
VGVCGKEGQSLPVGVGQPTLKLNLTVGGTA"

gene      complement(206318..2071 /locus-tag="y0194"
87)
CDS       complement(206318..2071 /locus-tag="y0194"
87)

/function="enzyme"
/note="residues 6 to 270 of 289
are 48.49 pct identical to
residues 4 to 266 of 275 from
GenPept : >gb|AAF93594.1|
(AE004129) conserved hypothetical
protein [Vibrio cholerae]"
/codon-start=1
/transl-table=11
/product="putative carbon-nitrogen
hydrolase"
/protein-id="AAM83788.1"
/db-xref="GI:21956866"
/translation="MKNANVALLQLCSGENTRDN
LAQIEQQIKQLNAGIKLVMTPENA
LLFANAASYRHAEHHNDGPLQQEVREMARYGV
WIQVGSMPMVSRESPDLITSSSL
FDDQGELKARYDKIHMFVDVDINDIHGHYRESDTY
QPGQQLTVVDTPVGRLGMTICYDL
RFPGLFQALRAQGAETISVPAAFTKMTGEAHWET
LLRARAIENQCVILAAQVGRHGA
TRRTWGHTMAVDAWGKIIGHNPDVAALKVRIET
AGLKTIRNQMPVMQHNRFQATLEP
TLNKPLLKPPSN"

gene      complement(207184..2103 /locus-tag="y0195"
75)
CDS       complement(207184..2103 /locus-tag="y0195"
75)

/note="residues 37 to 1062 of 1063
are 48.00 pct identical to
residues 1 to 985 of 986 from E.

```

coli K12 : B3245; residues 1 to
1056 of 1063 are 49.00 pct
identical to residues 244 to 1259
of 1266 from GenPept :
>gb|AAL22238.1| (AE008855) paral
putative protease [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83789.1"
/db-xref="GI:21956867"
/translation="MAAWLSIKSGEVYRGNVLLS
QGQANWTVGSNSHQLSVDNFVLEG
RRQGNGWQIDAPVLNLKTDGQAWPKGRLSALWLP
ENTQFIGPEQRQELRIRASNLQLE
RIGPLLPTLSPFTPELLARWADLQPQGYVDALAL
DIPISQPETTRFQAKWHDVSWQYW
GQLPGVNHFDGELSGSARLGRNLNINLKNSSLPYG
DLFRAPLEVSQASGALNWRIDDKG
WALWSDQLDVQAKSLWGNGSFYYMQPNQKPSQLN
QAQPWLKILAGIRLYDATDAWRYF
PVSLMGEKLADYLTEALQGGQVDNATLVYNGNP
DFPYKNKEGQFQVYVPLRNAVFQF
QPDWPALDNLAIDLNFLNEGLWMNAPHTLLGKVI
GSNISAIIPDYLKEKLYVDADVLG
EGRDVHDYFTATPLKDSVAETLDELQVGGKISGR
LHLDIPLEEESITHASGEVTLNNN
SLLVKPLQSQLENINGKFRFYDGNLESETLSANW
YGQPLTVNFTTKEQPKDFLVNVGL
QGDWLPKLPGVPSLAKMLSGSANWQKQKAVKL
PQHKGPDYQVDVSADLKKVSSHLP
SPLDKNSGQALPLHVQVNGGLEAFTLSGSAGNNN
AFNSQWLLQGEKVELARAIWQTDS
KKIPSLPDDKALVFKLPAIDGERWLALLAPELAT
AASPFAASFSSPSATSSTQPKIKG
SKTNVILPKRLTLQTPPELLVGGQAWHQTLQADP
LPSGMKITAKQEVDGSLLMADYG
PWHADLNYLYYNPQWGSREANNPLAQAVSQEPTV
LQKPQPPSGISFSDWPALQLRCKA
CWILGQNIGRVNADLTPKGSALILTNGLIEAGNG
RANITGQWQQDRAGDKTTLNIGLN
GPRIDETLSFFGLTTLIKNASFAINADLNWRGVP
WEPQINTLSGTLKGRLGKGQLTDL
GGGRAGQLRLVSFDALLRKLQLDFSDTFSRDFA
FDSIRSTATLKNVMSNDLVIDG
LAADIAMNGKVDLVKRQIAMEAVITPELSATVGV
ATAFAINPIVGAAVFAASKILGPL
WSKVSLIRYQITGSLDQPTIHEVLRQLKENEAP"

gene complement(211201..2126
70)

CDS complement(211201..2126
70) /locus-tag="y0196"
/gene="cafA"

/locus-tag="y0196"
/function="structural component;
cell division"
/note="residues 1 to 489 of 489
are 90.18 pct identical to
residues 7 to 495 of 495 from E.
coli K12 : B3247"
/codon-start=1

		/transl-table=11 /product="cytoplasmic filament protein" /protein-id="AAM83790.1" /db-xref="GI:21956869" /translation="MTAELLVNITPSETRVAYID GGILQEIHIEREAKRGIVGNIYKG RVSRVLPQMQAQAFVDIGLDKAAFLHASDIMPHE CVAGDEQKNFNVRDIAELVRQGQD LMVQVVKDPLGTGKARLTDDITLPSRYLVLMPGA AHVGVSQRIESEAEERERLKKTVAA YCDEQGGFIIRTAEGIGEEELSADAAFLKRLWT KVQERKKRNITKYKLYGEMALQR VLRDFAGAALDKIRVDSKLTLDLVEFTREYIPE MTDKLELYTGKQPIFDLYDVENEI QRSLEKVELKSGGYLIIDQTEAMTTVDINTGAF VGHRNLEETIFNTNIEATQAIARQ LRMRNLGGIIIIIDFIDMSNEDHRRRVLHSLEQAL SKDRVKTSINGFSQLGLVEMTRKR TRESIEHVLCHECPTCRGRGTVKSIVETVCYEILR EIVRVHHAYDSRFLVYASPAVGE ALKGEESHAAEVEIFVGKQVKVQIEPLYNQEQF DVVMM"
gene	complement (212660..213259)	/locus-tag="y0197"
CDS	complement (212660..213259)	/locus-tag="y0197"
		/note="residues 3 to 198 of 199 are 70.40 pct identical to residues 1 to 196 of 197 from E. coli K12 : B3248" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83791.1" /db-xref="GI:21956870" /translation="MPMTALYLASASPRRRELLA LLDLPFEVLKTEVEEQRHPGESAQ VYVQRLAQDKARAGVAVAPQDLPVLGADTIVVLN GQVLEKPRDKEHAQQILSALSGQK HQVMTAVALADRQNMLSAMVVTDVTFRVLSPLEI SDYIATGEPMDKAGAYGIQKGKGC FVRAIAGSYHAVVGLPLVETHELLSHFIAQRNVR GIHDS"
gene	212878..213480	/locus-tag="y0198"
CDS	212878..213480	/locus-tag="y0198" /note="residues 23 to 126 of 200 are 29.80 pct identical to residues 226 to 324 of 454 from GenPept : >gb AAF11838.1 AE002061-5 (AE002061) cell wall glycyl-glycine endopeptidase, putative [Deinococcus radiodurans]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83792.1" /db-xref="GI:21956871" /translation="MSHLSQPWPITCFADRPTPR RSSPDASGQTMHSVFVHVYPV


```

FLKPAHLTPQWYRHPVPVVRQPHLPVLYPAP
NAGHTPAHSRQGDAALQPLFSVPQ
TVNPTGPVIHGDDAKQKPDGQSWALNPYCTENW
RRILRISRNSHGQRMPLTTLLQKT
SGRNATLITKNSDQNTTTSIVSESSMTISACCHS
AILRNN"
gene      complement(213267..2137 /gene="mreD"
55)
CDS      complement(213267..2137 /gene="mreD"
55)
        /locus-tag="y0199"
        /function="structural component;
        murein sacculus, peptidoglycan"
        /note="residues 1 to 162 of 162
        are 75.30 pct identical to
        residues 1 to 162 of 162 from E.
        coli K12 : B3249; residues 4 to
        162 of 162 are 77.35 pct identical
        to residues 5 to 163 of 163 from
        GenPept : >gb|AAL22241.1|
        (AE008855) rod shape-determining
        protein [Salmonella typhimurium
        LT2]"
        /codon-start=1
        /transl-table=11
        /product="rod shape-determining
        protein"
        /protein-id="AAM83793.1"
        /db-xref="GI:21956872"
        /translation="MNRYSSHGRWVIWLSFLIAM
        VLQIMPWPEQIYMFRPSWLALVLI
        YWVMALPHRVNVGTGFILGLIMDLILGSTLGVRA
        LAFSIIAYLVAFKFQLFRNMALWQ
        QALIVMLLSLTMDVVVFWSEFLVINVAFRPEVFW
        SSVVNGILWPWFLFLMRKIRRQFS VQ"
gene      213735..213854
CDS      213735..213854
        /locus-tag="y0200"
        /locus-tag="y0200"
        /note="residues 2 to 38 of 39 are
        44.73 pct identical to residues 73
        to 110 of 118 from GenPept :
        >dbj|BAB47792.1| (AP002994)
        unknown protein [Mesorhizobium
        loti]"
        /codon-start=1
        /transl-table=11
        /product="hypothetical"
        /protein-id="AAM83794.1"
        /db-xref="GI:21956873"
        /translation="MTTVTIHGETPGVTTPGVAP
        AGVDAAGAGGPIASAEGNT"
gene      complement(213752..2147 /gene="mreC"
47)
CDS      complement(213752..2147 /gene="mreC"
47)
        /locus-tag="y0201"
        /locus-tag="y0201"
        /function="structural component;
        murein sacculus, peptidoglycan"
        /note="residues 1 to 316 of 331
        are 81.32 pct identical to
        residues 1 to 316 of 367 from E.

```

		coli K12 : B3250; residues 1 to 327 of 331 are 80.30 pct identical to residues 1 to 330 of 350 from GenPept : >emb CAD07888.1 (AL627278) rod shape-determining protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="rod shape-determining protein" /protein-id="AAM83795.1" /db-xref="GI:21956874" /translation="MKPIFSRGPSLQLRLFFAII AAIVLVIADSRLGTFVKIRTYMDT AVSPFYFLANGPRKILDNVSDTLATREQLELENR ALRQELLLKNTDLQLLGQFKQENN RLRELLGSPLRQDEQKMVTQVMSSGTDYPYSDHVV IDKGSNSGVYEGQPVISDRGVVGQ VVAVSKFTSRVLLICDASHALPIQVLRNDIRVIA AGSGCSDDLLEHLPSNTDIRVGD VLVTSGLGGRFPEGYPVAVVSSVKVDNQRAYTVI QARPTADLQRLRYLLLLWGADRNG DMPMPPEVRRVANERLAPMMSQVLPSADAMGPP APAASTPAGATPGVVTGPVSP"
gene	complement (214951..2159 94)	/gene="mreB"
CDS	complement (214951..2159 94)	/locus-tag="y0202" /gene="mreB" /locus-tag="y0202" /function="phenotype; cell division" /note="septation function; residues 1 to 347 of 347 are 99.13 pct identical to residues 21 to 367 of 367 from E. coli K12 : B3251; residues 1 to 347 of 347 are 100.00 pct identical to residues 1 to 347 of 347 from GenPept : >emb CAC93135.1 (AJ414158) rod shape-determining protein MreB [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="regulator of ftsI, penicillin binding protein 3" /protein-id="AAM83796.1" /db-xref="GI:21956875" /translation="MFKKFRGMFSNDLSIDLGTA NTLIYVKQGQIVLNEPSVVAIRQD RAGSPKSVAAVGHDAKQMLGRTPGNIAAIRPMKD GVIADFFVTEKMLQHFIKQVHSNS FMRPSPRVLVCPVVGATQVERRAIRESAQGAGAR EVFLIEEPMAAAIGAGLPVSEATG SMVVDIGGGTTEVAVISLNGVVYSSSVRIGGDRF DEAIINYVRRNYGSLIGEATAERI KHSIGSAYPGDEVLEIEVVRGNLAEGVPRGFTLN SNEILEALQEPLTGIVSAVMVALE QCPPELASDISERGMVLTGGGALLRNLDRLLMEE TGIPVVVAEDPLTCVARGGGKALE MIDMHGGDLFSEE"

gene	complement(216331..2182 /locus-tag="y0203"	
	47)	
CDS	complement(216331..2182 /locus-tag="y0203"	
	47)	/note="residues 1 to 638 of 638 are 50.70 pct identical to residues 1 to 641 of 646 from E. coli K12 : B3252; residues 1 to 638 of 638 are 50.70 pct identical to residues 1 to 641 of 646 from GenPept : >gb AAG58379.1 AE005553-1 (AE005553) orf, hypothetical protein [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83797.1" /db-xref="GI:21956876" /translation="MRFTTKLSAFMTLLVVLAMC LVLLGSTISFFYLCQKKMEQRLQS IVTAYDQSLLLQPINKKREWLPLMMQTLGVVDVS VKNSTSTLYQLHIPAVYTPWNSHS RYRQMVLPLLHQPGTEMHFNYIDPLGSYARSIYA AAILSLVVVVIALTLLLSFRWLRD QTVGQEKLERRARRILNGEREHAVRSEDYEWPPC ASRAIDHLLSELMEVRAERNRVDI LIRTFAAQDAQTGLSNRQFFDNQLTTQLEETGAH GVVMMVQLPDFEALNETHDQQQVQ ELMSSLVNLLSTFVARYPSALLARYLNSDIAILL PHKTLKDADVMAAQLVNAVRTLPE PHIIDRESLLHIGIVAYRSGESVEQIMDNAGQAT KSAALYGGNGWYVFDITQVPERGRG SVKWRITLLEQTLASGGPRLYQKPVITVDGKISHR EIISRIYDGEQEELAAEFMPLVQL LGLGERYDRQKIDKIIPLLSLWPDETAFSISVD SLLHRPFQRWLRDITLLQCKKSDRM RIIFELAEADVQCQHIEEIRQMVRLLRGVGCKVMA SQAGLTVVSTSYIKSLQVEMIKLH PGVVRSINFRYENQLFVESLTGACAGTQTKVFAA EVRTREEWQTLQEKGVYGGQGNFF APPTPLNSGKKKYS" /locus-tag="y0204" /locus-tag="y0204" /note="residues 1 to 324 of 325 are 74.38 pct identical to residues 1 to 323 of 324 from E. coli K12 : B3253; residues 1 to 324 of 325 are 74.69 pct identical to residues 1 to 323 of 324 from GenPept : >gb AAG58380.1 AE005553-2 (AE005553) putative dehydrogenase [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative dehydrogenase" /protein-id="AAM83798.1" /db-xref="GI:21956877" /translation="MRALILEQIEGRTTAEVRQI SASQLPAGNVTVDVNWSSLNYKDA
gene	218648..219625	
CDS	218648..219625	

gene	219764..220948	LAITGQGKIIRQFPMVPGIDFAGTVHSSSEDPRFH
CDS	219764..220948	IGQSVLLTGWGVGENHWGGLAEQA
		RVNGDWLVMPMPDGLDARKAMIIGTAGFTAMLCVM
		ALEDGGVTPKSGEVVVTGASGGVG
		STAIALLSALGYQIAAISGRDSNSDYLKNLGAQR
		ILPRSDYLDASRPLEKQLWAG AID
		TVGDSMLAKILAQMNYNGTVAACGLAGGYNLPTT
		VMPFILRNIRLQGVDSVMT PQPR
		LQAWQRLQKILPESFYQQASQAITLADTPTIAAR
		LLANEVTGRTL VKVR"
		/locus-tag="y0205"
		/locus-tag="y0205"
		/note="residues 62 to 394 of 394
		are 75.44 pct identical to
		residues 1 to 334 of 334 from E.
		coli K12 : B1971; residues 62 to
		394 of 394 are 79.04 pct identical
		to residues 1 to 334 of 334 from
		GenPept : >gb AAL22246.1
		(AE008855) putative nitrate
		reductase [Salmonella typhimurium
		LT2]"
		/codon-start=1
		/transl-table=11
		/product="putative reductase"
		/protein-id="AAM83799.1"
		/db-xref="GI:21956878"
		/translation="MFPFATMINHIRGNAINDIK
		GNYPTESAMHNTFTHTKNNTHTKN
		NTQAKNSGSQTKSNAVSLNKPRKLTEADVTPESI
		FYQRRKVLQALGITAATLALPASA
		QADLLAWFKGNEPPKAPSGKPLTFTPSAAYHPDL
		ALTPEDKVTGYNNFYEFGLDKADP
		AANAGTLKTEDWQIKIDGDVVKPMTLDMDYLMKC
		FPLEERIYRLRCVEAWSMVVPWIG
		FELGKLLKLAEPTSNARYVAFQTLYAPDQMPGQK
		NRFIGGGLDYPYVEGLRLDEAMHP
		LAFMVVG VYGKTLPPQNGAPLRLMTPWKYGFKSI
		KSIVHIRLTRDQPPTTWNLSAPNE
		YGFYANVNPHVDHPRWSQATERVIGSGGILDVKR
		QPTLLFNGYAEQVASLYRGLDLRK NF"
gene	220948..221568	/locus-tag="y0206"
CDS	220948..221568	/locus-tag="y0206"
		/note="residues 1 to 203 of 206
		are 68.96 pct identical to
		residues 1 to 203 of 211 from E.
		coli K12 : B1972; residues 1 to
		206 of 206 are 72.81 pct identical
		to residues 1 to 199 of 199 from
		GenPept : >emb CAD07893.1
		(AL627278) putative membrane
		protein [Salmonella enterica
		subsp. enterica serovar Typhi]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83800.1"
		/db-xref="GI:21956879"
		/translation="MRLSLRHITWLKIAIWLAAT
		LPLLWLVL SINLGGLSADPAKDIQ
		HFTGRMALKLLLATLLVSPLARYSKQPLLLRCRR
		LLGLWCFAWGTLHLLSYSILELGL

		SNIGLLGHELINRPYLTLGIISWLVLLALALTST RWAQRKMGARWQKLHNWVYVVAIL APIHYLWSVKTLSPWPPIIYAVMAALLLLLRYKLL LPRYKKFRQWFR"
gene	221831..222283	/locus-tag="y0207"
CDS	221831..222283	/locus-tag="y0207" /function="enzyme" /note="residues 1 to 146 of 150 are 73.28 pct identical to residues 1 to 146 of 149 from GenPept : >gb AAD10235.1 (AF011408) type II 3-dehydroquinase [Aeromonas salmonicida subsp. salmonicida]" /codon-start=1 /transl-table=11 /product="putative dehydroquinase" /protein-id="AAM83801.1" /db-xref="GI:21956881" /translation="MSDKFHILLNLPNLLGTL REPEKYGYTTLAEIVSQLEIQAQG MDVALSHLQSNAEHALIDSIHQARGNTDFILINP AAFTHTSVALRDALLGVQIPFIEI HLSNVHAREPFRHHSYLSDIAGVICGLGADGYN FALQAAVNRLSKSN"
gene	222396..222905	/gene="accB"
CDS	222396..222905	/locus-tag="y0208" /gene="accB" /locus-tag="y0208" /function="carrier; biosynthesis of cofactors, carriers: biotin carboxyl carrier protein (BCCP)" /note="carrier of biotin; residues 16 to 169 of 169 are 82.80 pct identical to residues 1 to 156 of 156 from E. coli K12 : B3255; residues 16 to 169 of 169 are 82.80 pct identical to residues 1 to 156 of 156 from GenPept : >gb AAL22248.1 (AE008856) acetylCoA carboxylase, BCCP subunit, carrier of biotin [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="acetyl CoA carboxylase, BCCP subunit" /protein-id="AAM83802.1" /db-xref="GI:21956882" /translation="MMGIIATHKEYGITLMDIRK IKKLIELVEESGISELEISEGEES VRISRAPAAPNYPMMQQPYAFAAPQQPALAAAV APAPVAEAAPAAISGHIVCSPMVG TFYHTSPDAKAFVEVGQKVSVDLTLGIVEAMKM MNQIEADKSGTVKAILVENGQPVE FDEPLVVIE"
gene	222917..224266	/gene="accC"
CDS	222917..224266	/locus-tag="y0209" /gene="accC" /locus-tag="y0209" /function="enzyme; fatty acid and phosphatidic acid biosynthesis"

		/note="residues 1 to 448 of 449 are 92.41 pct identical to residues 1 to 448 of 449 from E. coli K12 : B3256" /codon-start=1 /transl-table=11 /product="acetyl CoA carboxylase, biotin carboxylase subunit" /protein-id="AAM83803.1" /db-xref="GI:21956883" /translation="MLDKIVIANRGEIALRILRA CKELGIKTVAVHSVADRD LKHVLL ADETV CIGPAPSVKSYLNIPAIISAAEITGAVAV HPGYGFLSENADFAEQVERSGFIF IGPRAETIRLMGDKVSAISAMKKAGVPCVPGSDG PLSDDTTKNKAF AKRIGYPV IKA SGGGGGRGMRVVRHDKDLEESINMTRAEAKAAFN NDMVYMEKYLENPRHIEVQILADG QGNAIYLAERDCSMQRRHQKVVEEAPAPGITSEM RRYIGERCAKACMEIGYRGAGTFE FLYENGEFYFIEMNTRI QVEHTVTEMITGIDLIK EQLRIAAGQPLSIKQDEVKVHGH A VECRINAEDPNTFLPSPGKITRFHAPGGFGVRWE SHIYAGYTVPPYYDSMIGKLITYG ENRDVAIARMKNALAE L IIDGIKTNVELQQRIMN DENFQHGGTNIHYLEKKLGLQET" /locus-tag="y0210" /locus-tag="y0210" /note="residues 1 to 79 of 80 are 68.35 pct identical to residues 1 to 79 of 80 from E. coli K12 : B3257; residues 1 to 79 of 80 are 69.62 pct identical to residues 1 to 79 of 80 from GenPept : >gb AAG58385.1 AE005553-7 (AE005553) orf, hypothetical protein [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83804.1" /db-xref="GI:21956884" /translation="METRFLQANKEARWAFGLTL AYLAGWIITAYLPGNLPGMSGLPA WFEAACIALPLLFI VLCILMVRLIFRDIPLEDD AN" /gene="panF" /locus-tag="y0211" /gene="panF" /locus-tag="y0211" /function="transport; transport of small molecules; cations" /note="residues 1 to 472 of 486 are 82.83 pct identical to residues 1 to 472 of 485 from E. coli K12 : B3258" /codon-start=1 /transl-table=11 /product="sodium/pantothenate symporter" /protein-id="AAM83805.1"
gene	225624..225866	
CDS	225624..225866	
gene	225850..227310	
CDS	225850..227310	

		/db-xref="GI:21956885" /translation="MTMQTDVVLPLVGYLVLVFG LSIYAYTRRQTGNFLNEYFIGNRS MGGFVLAMTLTATYISASSFIGGPGAAYKYGLGW VLLAMIQLPAVWLSLGVLGKKFAI LARRYNAVTLNDMLYARYQSRLLVWLASISLLVA FVGAMTVQFIGGARLLETAAGIPY DTGLLIFGISIALYTSFGGFRASVLNDALQGLVM LIGTILLVAVIHAAGGLHKAVET LQHIDPALVSPQGGDQILDVPFMASFWILVCFGV IGLPHTAVRCISYRDSKAVHRGII LGTIVVAILMFGMHLAGALGRAVLPDLKIPDQVI PTLMITVLPPFAAGIFLAAPMAAI MSTINAQLLQSSATIVKDLYLNLWPAELKNERKL ARISLSTLILGLLLLLLAAWRPPE MIIWLNLLAFGGLEAVFLWPLVLGLYWERANAHG ALSAMIVGAVCYTVLASFDIKIAG LHPIVPSLTLNLLAFYIGNLFGDRARARHPAIVS AD"
gene	227347..228267	/gene="prmA"
		/locus-tag="y0212"
CDS	227347..228267	/gene="prmA" /locus-tag="y0212" /function="enzyme; ribosomal proteins - synthesis, modification" /note="residues 14 to 305 of 306 are 85.27 pct identical to residues 1 to 292 of 293 from E. coli K12 : B3259" /codon-start=1 /transl-table=11 /product="methylase for 50S ribosomal subunit protein L11" /protein-id="AAM83806.1" /db-xref="GI:21956886" /translation="MVMAPIPALERIAMPWIQLK LNTTGNQAESLGDVLVESGAVSVT FQDTHDNPVFEPLPGETRLWGD TDVIGLYDAETD MADVVAMLECHPQIGKGFHKIEQ LEDKDWEREWMDNFHMPRFGERLWICPSWRDVPD PTAVNVMLDPGLAFGTGTHPTTAL CLQWLDSLNLNGKTLIDFGCGSGILAI AALKLGA ARAIGIDIDPQAIQASRDNAQRNG VSERLELYLAKDQPAELSADV VVANILAGPLREL APLISVLPTTGHLGLSGVLATQA AGVAQAYEDKFILDPVAEKEEWCRITGIKK"
gene	228754..229821	/locus-tag="y0213"
CDS	228754..229821	/locus-tag="y0213" /note="residues 35 to 355 of 355 are 87.85 pct identical to residues 1 to 321 of 321 from E. coli K12 : B3260; residues 35 to 355 of 355 are 92.21 pct identical to residues 1 to 321 of 334 from GenPept : >gb AAC77880.1 (AF040378) yhdG homolog [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="putative dehydrogenase" /protein-id="AAM83807.1"

		/db-xref="GI:21956887" /translation="MLFFHQLVKVWPFIIWAQKCV IYAPLRTQCGHSLSMRIGHFQLTN CLIAAPMAGITDRPFALCHGMGAGMAVSEMLSS NPEVWRTDKSRLRMVHVDEPGIRN VQIAGNDPDEMAAAARINVASGAQIIDINMGCPA KKVNRKLAGSALLQHPDLVKQILS AVVNAVDPVPTLTKIRTGWSPEHRNCIEIAQLAEN CGIQALTIHGRTRSCLFNGEAEYD SIRAVKQTVSIPVIANGDITDPHKARAVLDYTGA DALMIGRAAQGRPWFIREIQHYLD TGELLPPMPLGEVQRLLDGHIRELHDFYGPCKGF RIARKHVSWYLQEHAPNDQFRRTF NAIEDASEQLEALEAYFENLA"
gene	229846..230142	/gene="fis"
CDS	229846..230142	/locus-tag="y0214" /gene="fis" /locus-tag="y0214" /function="factor; DNA - replication, repair, restriction/modification" /note="DNA-binding protein; a trans activator for transcription; residues 1 to 98 of 98 are 97.95 pct identical to residues 1 to 98 of 98 from E. coli K12 : B3261" /codon-start=1 /transl-table=11 /product="site-specific DNA inversion stimulation factor" /protein-id="AAM83808.1" /db-xref="GI:21956888" /translation="MFEQRVNSDVLTVATVNSQD QVTQKPLRDSVKQALKNYFAQLNG QDVSDLYELVLAEEVEQPLLDMMVMQYTRGNQTRAA LMMGINRGTLRKKLKKYGMN"
gene	complement(230896..231372)	/locus-tag="y0215"
CDS	complement(230896..231372)	/locus-tag="y0215" /note="residues 13 to 88 of 158 are 33.70 pct identical to residues 4 to 89 of 134 from GenPept : >dbj BAB04617.1 (AP001510) BH0898 unknown conserved protein in B. subtilis [Bacillus halodurans]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83809.1" /db-xref="GI:21956889" /translation="MNTENKKLSTLIGKIHTIAK SRLAAGYEDRNGINEHQVTPCHHA LTLGGDDFAESYLPFLRVNGFDLNGVRLFGYF DDKGDERDLRKQLADLKAPELFP DAFNDWVLIGETDITDILIFNKKNGSYENRDRIGL DRLNESYDDIVGLLISLMPLIE"
gene	complement(231438..232163)	/locus-tag="y0216"
CDS	complement(231438..232163)	/locus-tag="y0216"


```

/function="regulator"
/notes="residues 29 to 231 of 241
are 36.71 pct identical to
residues 9 to 215 of 223 from
GenPept : >dbj|BAB53015.1|
(AP003010) transcriptional
regulator [Mesorhizobium loti]"
/codon-start=1
/transl-table=11
/product="putative transcriptional
regulator"
/protein-id="AAM83810.1"
/db-xref="GI:21956890"
/translation="MFCITEAWYKKQPYCRTGIQ
LMLAGMGVIKPETLRYQVENVLRQ
AIMSGRFTPGERLIERELCETLGVSRTSIREALR
RLEAEKLVSIVPHKGPIVAIISRQ
EAAELFALRGLLEGFAAREFAQRATDVAIVHFAQ
AIQALRMAGMTKDRAKVLKAKTDL
YDVLLDNCNGNLVKETLTSLSHRINLLRATSLMD
PQRLPVSINEIDDLQALKARPD
AAERHVANAKEVALRILEETNAT"
gene      complement(232190..2335 /locus-tag="y0217"
54)
CDS       complement(232190..2335 /locus-tag="y0217"
54)

/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/notes="residues 31 to 444 of 454
are 26.35 pct identical to
residues 35 to 452 of 461 from
GenPept : >dbj|BAB60327.1|
(AP000995) shikimate transporter
[Thermoplasma volcanium]"
/codon-start=1
/transl-table=11
/product="putative metabolite
transport protein, permease"
/protein-id="AAM83811.1"
/db-xref="GI:21956891"
/translation="METLSADSAITAAENDPLRD
VKRKNAIKGAFFSEFIDMFDIYLP
VIVLPPVLFFYFQPPNLSSTANILASLVFITLL
GRPIGALLFGIMADRIGRRMASIY
SVSGFGVVTFLIALIPGYETLGIASYLLLVLLRF
IDGIFLGGGYTGAIPLALEYSKKE
QRGFVGGILILSGFPAAYVAINLVAMLMFALIPLD
GLYSPYAQWGWRIPFVIGGLLAGF
LALYYVFNVTSEVWQQGSSKKRAREKQPLSTLV
SGQSGRNLWQVLLMMSGFWLTQNL
ITLFLPTGLLINTLNMRGLQVTSILLVTYCVLFF
SYIGMGMGLGQKIGRRRFFMIAGPL
IATMGSALLYVLSHGDGLSFSTVMLLVCLLAVVV
TSPWGVIIITYINEHFATGVRATGF
GVGFSLSVIIPSFYAFYMDWLSVVVPFELTAVVL
LALGGMIGTVGAIMPETKEVDFT SSAG"
gene      complement(233708..2341 /locus-tag="y0218"
45)
CDS       complement(233708..2341 /locus-tag="y0218"
45)

/function="enzyme"

```

```

/feature "note" {
    /text="residues 21 to 141 of 145
are 48.36 pct identical to
residues 15 to 136 of 139 from
GenPept : >gb|AAK42990.1|
(AE006881) 4-carboxymucolactone
decarboxylase (pcaC) [Sulfolobus
solfataricus]"
    /codon-start=1
    /transl-table=11
    /product="putative decarboxylase"
    /protein-id="AAM83812.1"
    /db-xref="GI:21956893"
    /translation="MSNRVGYEIGRRVMMVAQDR
FERGFHNRKVVLGAEHVETSWGNS
DEFNRPVQKLITEYCWGEVWGDPAITFKTRSMNLN
IGILTAMGQHHELSTLHVKGALRNG
VTREEIRAVLLQTVVYCGAPVALAAFRISAAIK
AYDDEIADS"
}

gene complement(234281..2351 /locus-tag="y0219"
71)
CDS complement(234281..2351 /locus-tag="y0219"
71)

/feature "note" {
    /text="residues 6 to 290 of 296
are 34.58 pct identical to
residues 2 to 290 of 298 from
GenPept : >emb|CAD17800.1|
(AL646080) probable
3-hydroxyisobutyrate dehydrogenase
oxidoreductase protein [Ralstonia
solanacearum]"
    /codon-start=1
    /transl-table=11
    /product="putative oxidoreductase"
    /protein-id="AAM83813.1"
    /db-xref="GI:21956894"
    /translation="MKQLQRIGFIGLGKMGTPMV
QRLVKAGFELYLCDADITKVQILT
AELNAESLTVDNAASLDALITMLPNSEAVEQVLL
GSDGISGWVAQLSQAVIDMSSS
DPERSRRLAILLAVWELDYLDAPVSGGVKKAQNG
TSLILIGGEDRVLKSCYTALAAMG
EQILFVGPAGSGHAAKALNNYVSATGLLATIEAL
HVAQRFGIEPEVMTEVLNTSTGRS
NTSENKVRQFMLNGSYASGFTLQLMNKDLHIARN
LAQRLNYPMRLGMHCVDVWDEVSR
RATPMADHTEMYRLLIDKEP"
}

gene complement(235236..2360 /locus-tag="y0220"
63)
CDS complement(235236..2360 /locus-tag="y0220"
63)

/feature "note" {
    /text="residues 46 to 246 of 275
are 28.20 pct identical to
residues 34 to 254 of 262 from
GenPept : >gb|AAB89741.1|
(AE000998) A. fulgidus predicted
coding region AF1509
[Archaeoglobus fulgidus]"
    /codon-start=1
    /transl-table=11
    /product="hypothetical"
    /protein-id="AAM83814.1"
}

```

		/db-xref="GI:21956895" /translation="MENRDMSASHENYRIFAICY AHHHRLTRDNFLGGDPHDGMPID YFVVAIVGTTRTIMVDTGFDAAMAHQGRGTITHC IEDGLSQLGIDAGKIEDVISHMH YDHAGNHGLFPNARFHLQDREMAFCTGRCMGHHG LSQAFDVEDVKAMVGRLFAGRLQF HHGDAEIAPGISVHRVGGHTDGLQIIRVHTARGW VVLASDATHFYANIQQRRPYPILY NVGDVLEGYNTLYRWADSFHIIIPGHDPMLQRY PAGTPETAAWIAQVDVAPLTQWT"
gene	236518..236991	/gene="slyB"
CDS	236518..236991	/locus-tag="y0221" /gene="slyB" /locus-tag="y0221" /function="putative membrane" /note="residues 3 to 157 of 157 are 66.02 pct identical to residues 1 to 155 of 155 from E. coli K12 : B1641; residues 3 to 157 of 157 are 73.71 pct identical to residues 1 to 155 of 155 from GenPept : >emb CAA42977.1 (X60448) outer membrane lipoprotein [Yersinia enterocolitica]" /codon-start=1 /transl-table=11 /product="putative outer membrane receptor" /protein-id="AAM83815.1" /db-xref="GI:21956896" /translation="MIMNKLAI VALAATVLSGC ANNTASGDTFTASQARQVQTVTYG SIVSARPVTIQGGNNNNVAGAIGGAVVGGFLGNT IGGGRGNSLATAGGAVAGGVAGQG IQSAMNRSEGVQLEIRDDGSNIVVVQAQGPTRF SAGQRVIIASDRSGTVTVSPR"
gene	complement(237082..237279)	/locus-tag="y0222"
CDS	complement(237082..237279)	/locus-tag="y0222" /note="residues 41 to 57 of 65 are 76.47 pct identical to residues 1185 to 1201 of 1247 from GenPept : >gb AAL20679.1 (AE008778) nitrate reductase 1, alpha subunit [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83816.1" /db-xref="GI:21956897" /translation="MVFSSDFMGYVLHLMWINNL LRQLNACGNLCNIFGGGRAYHHFV THISPKPTHMIGGLRAISLRL"
gene	237428..237736	/gene="cspI"
CDS	237428..237736	/locus-tag="y0223" /gene="cspI" /locus-tag="y0223" /function="phenotype; Not classified"

		/note="residues 33 to 102 of 102 are 82.85 pct identical to residues 1 to 70 of 70 from E. coli K12 : B1552; residues 33 to 102 of 102 are 98.57 pct identical to residues 1 to 70 of 70 from GenPept : >emb CAB10779.1 (Z97978) hypothetical protein [Yersinia pestis]"
		/codon-start=1 /transl-table=11 /product="cold shock-like protein" /protein-id="AAM83817.1" /db-xref="GI:21956898" /translation="MSLLLSAQVRHPLKDRPRSL HYCGKIIIEGNISMSNKMTGLVKWF DAGKGFGITPADGSKDVFVHFSAIQSNDFKTLDE GQNVEFSIENGAKGPSAVNVIAL "
gene	237921..238208	/gene="cspI"
		/locus-tag="y0224"
CDS	237921..238208	/gene="cspI"
		/locus-tag="y0224"
		/function="phenotype; Not classified"
		/note="residues 26 to 95 of 95 are 84.28 pct identical to residues 1 to 70 of 70 from E. coli K12 : B1552; residues 26 to 95 of 95 are 100.00 pct identical to residues 1 to 70 of 70 from GenPept : >emb CAB10779.1 (Z97978) hypothetical protein [Yersinia pestis]"
		/codon-start=1 /transl-table=11 /product="cold shock-like protein" /protein-id="AAM83818.1" /db-xref="GI:21956899" /translation="MPHKFYPSLSSRLWRQLKII EGSISMSNKMTGLVKWFDAGKGFG FITPADGSKDVFVHFSAIQSNDFKTLDEGQNVEF SIENGAKGPAAVNVIAL"
repeat-region	complement(238285..2389 94)	/note="insertion element"
		/insertion-seq="IS1541a"
gene	complement(238391..2389 00)	/locus-tag="y0225"
CDS	complement(238391..2389 00)	/locus-tag="y0225"
		/function="IS and transposon related functions" /note="IS1541a; residues 1 to 169 of 169 are 100.00 pct identical to residues 1 to 169 of 169 from GenPept : >gb AAC82673.1 (AF074611) transposase [Yersinia pestis]"
		/codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83819.1" /db-xref="GI:21956900"

gene	238849..239211	/translation="MRSGNCKCSTRNQKGVPMRD EKSLAHTRWNCKYHIVFAPKYRRQ VFYREKRRAIGSILRKLCEWKNVNILEAEYCVDH IHMLLEIPPKMSVSGFMGYLKGKS SLMLYEQFGDLKFKYRNREFWCRGYVDTVGNKNT ARIQEYIKHQLEEDKMGEQLSIPY PGSPFTGRK"
CDS	238849..239211	/locus-tag="y0226" /locus-tag="y0226" /note="residues 61 to 115 of 120 are 36.36 pct identical to residues 30 to 81 of 275 from GenPept : >gb AAL48672.1 (AY071050) RE13795p [Drosophila melanogaster]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83820.1" /db-xref="GI:21956901" /translation="MGPPFDLLNICSCQTANCF NKSKGVFITDPKLKALLNPQPSWG FSGHKKNLPPCRFFCAYDTGTDIKNTALPRAPES PADIIAAQKNHVTGQETVIWLNLYL TILAGSPFIHLEQCETVV"
gene	239254..240429	/locus-tag="y0227"
CDS	239254..240429	/locus-tag="y0227" /note="residues 1 to 388 of 391 are 58.50 pct identical to residues 1 to 388 of 391 from GenPept : >gb AAL19518.1 (AE008722) putative ATPase involved in DNA repair [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83821.1" /db-xref="GI:21956902" /translation="MKKLIKRLIIEIKSGIELEDD DIIRHQLPYLKSETQDPVLVFIVM AIEQGKFTQALDAIATWLGSKQGVQWQDIELAA CKLELKALEEQLSELIDKRNERIQ LLDDFNDLYLVRLGPLMKQILNLRQLAESTLRK AEAEARRRERDYRNCQQYISQAID ELISLKQRWLALPSISNDTIEIRNRIQQQTELIT ALLAEIKELENSFCTRNTSTRKA REEAKEKYERYQEQQTDAEQRLDNDRKLSSSEQRQ DLKRLWRQASRLCHPDLVADAFKE KAHQLMVQLNQARQRGDFPAIHALLESKQGLEP LMASDLIDDLERLRKISDVRTQI DAILHEIDALKGEESWRLATSLPKDKWFKEQEN VLSKTLNILERQVEEASRVLYEA"
gene	complement(240536..2418 82)	/locus-tag="y0228"
CDS	complement(240536..2418 82)	/locus-tag="y0228" /note="residues 3 to 446 of 448 are 52.78 pct identical to residues 1 to 449 of 452 from GenPept : >emb CAC45768.1 (AL591786) hypothetical signal

		peptide protein [Sinorhizobium meliloti]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83822.1"
		/db-xref="GI:21956903"
		/translation="MHMSKFRLVLLASSIAFSTS SWAQAVEVPAVLAGHAVLPVKSTV ATPSDAPTDLQQSGKYTSGQRVSALGSVAAKSAD RLTGIGLPISGQPLQGHSGIKHMP DGTYWVLTDNGFGSKANSPDAMLYLNHYNIDFKN GNVTPLQTVFLHDPDKKVPFHIIN ESTEKRYLTGSDFDPESFQFADDALWIGDEFGPY LIKADLNGKVLAVFETQVDGNVVK SPDNPTLTLPGAPDGKQNFQVARSKGFEGMAVSP DGSKLYPELEGALWDGEKFENIDG KRYLRVLEFDVKNQAWTGRSWQYVLEDNQNAIGD FNLIDANHGLVIERDNGETADKA CAAGAPTDKCFSQIAKFKRVIKIAFSDDNVGKPV EKVSYIDLLNIKDPQNLARKPLNN GVLTFPFFFTIENVVDVVDASHIIVGNDNNFPFSSS RQPNEADDNEFILLDVKALLSQ"
gene	242133..242987	/locus-tag="y0229"
CDS	242133..242987	/locus-tag="y0229"
		/note="residues 2 to 280 of 284 are 70.25 pct identical to residues 17 to 295 of 304 from E. coli K12 : B2989; residues 2 to 280 of 284 are 72.04 pct identical to residues 1 to 279 of 288 from GenPept : >gb AAL22014.1 (AE008844) putative glutathione S-transferase [Salmonella typhimurium LT2]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical protein"
		/protein-id="AAM83823.1"
		/db-xref="GI:21956904"
		/translation="MMKDNEYQPPKIWTENNASG GVWSKINRPTAGARYEADLPVGKH PLQLYSMGTPNGQKVTTILLEELLALGEKGAEYDA HLIRISEGEQFSSGFVSINPNSKI PALMDYSSTPPVRVFESGAILLYLADKFGHFLPK SHAARTEALNWLFWLQGAAPYLGG GFGHFYHYAPVKIEYAI DRFTMEAKRQLDLLNTQ LKTHEYIAGDEYTIADIAIWPWYG SLVLGLQYEAGEFLDVKSYPHLIRWTETIAKRPA VQRGRIVNRTWGAPEEQ LPERHDA ADFDRLIK"
gene	complement(243177..243782)	/locus-tag="y0230"
CDS	complement(243177..243782)	/locus-tag="y0230"
		/note="residues 14 to 194 of 201 are 44.75 pct identical to residues 14 to 194 of 200 from GenPept : >emb CAC95734.1 (AL596165) similar to putative sugar-phosphate isomerase [Listeria innocua]"
		/codon-start=1

```

/translation="MSQNKEWLAASDAWMIYSRE
LAALKENVDQQVWLQVLDALAECR
GKIAVTGVTSGIAARKVAHMLACVEQPAIYLNA
TDAAHGDLGFLGAQDIIILISRG
NSDELTRLPTLQRKQVKIISVTENEQSAIAQVS
ALVLKTHVKQEIDPLNMLATTSIV
LVLALFDAICACLMARTGFSKETLLAVHPGGDVG
MVLRKQQ"
gene      complement(243779..2454 /locus-tag="y0231"
31)
CDS      complement(243779..2454 /locus-tag="y0231"
31)

/function="enzyme"
/note="residues 8 to 548 of 550
are 50.44 pct identical to
residues 13 to 566 of 569 from
GenPept : >emb|CAB81024.1|
(AL161576) putative protein
[Arabidopsis thaliana]"
/codon-start=1
/transl-table=11
/product="putative sugar kinase"
/protein-id="AAM83825.1"
/db-xref="GI:21956907"
/translation="MRDKTMASYFIGVDVGTGSA
RAGVFDLQGRMVGQASREITMFKP
KADFVEQSSSENIWQAVCNAVRAVNQADINPIQV
KGLGFDATCSLVVLDKEGNPLTVS
PSGRNEQNVIVWMDHRAITQAERINATKHPVLEF
VGGVISPEMQTPKLLWLKQHMPNT
WSNVGHFLFDLPDFLTWRATKDETRSLCSTVCKWT
YLGHEDRWDPSTYFKLVGLADLLDN
NAAKIGATVKPMGAPLGHGLSQRAASEMGLIPGT
AVSVSIIDAHAGTIGILGASGVTG
ENANFDRRIALIGGTSTAHMAMSRSAHFISGIWG
PYYSAILPEYWLNEGGQSATGALI
DHIIQSHPCYPALLEQAKNKGETIYEALNYILRQ
MAGEPENIAFLTNDIHMLPYFHGN
RSPRANPNLTGIITGLKLSTTPEDMALRYLATIQ
ALALGTRHIIETMNQNGYNIDTMM
ASGGGTKNPIFVQEHANATGCAMLLPEESEAMLL
GSAMMGTVAAAGVFESLPEAMAAMS
RIGKTVTPQTNKIKAYYDRKYRVFHHQMYHDMRY
QALMQEGA"
gene      complement(245435..2463 /locus-tag="y0232"
88)
CDS      complement(245435..2463 /locus-tag="y0232"
88)

/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 20 to 310 of 317
are 58.76 pct identical to
residues 16 to 306 of 318 from
GenPept :
>gb|AAG54673.1|AE005211-8
(AE005211) putative permease
component of transport system,
```

		probably ribose specific [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative permease of ABC transporter" /protein-id="AAM83826.1" /db-xref="GI:21956908" /translation="MTWLNRTIPDDRIIRLQLLI LIAVMLVFSLTGQRFFSLGNFQS MSSQLPILGMLALGMGLTMTGGINLSIIAGANA CSLVMAAIIIVSHPGQPAFLLLALV AGLLVAVAIGTLNGVLISVIGVSPILATLGTMTL ITGLNILLSNGDVISGFPPVIQYI GSGDIVGIPVAMILFLLVAAGLWVLEHTTLGRS IYLVGSNEQATRFSGVNTHRVQIA VYILSALLGWGAAILMMAKFNSAKAGYGESYLLV TILASVLGGINPDGGFGRIIGLIL ALVVLQLLESGLNLLGVSSYLTMALWGGVLILFI ALQNRKA"
gene	complement (246390..2473 79)	/locus-tag="y0233"
CDS	complement (246390..2473 79)	/function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="residues 6 to 321 of 329 are 57.59 pct identical to residues 1 to 316 of 323 from GenPept : >gb AAG54672.1 AE005211-7 (AE005211) putative permease component of transport system, probably ribose specific [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative permease of ABC transporter" /protein-id="AAM83827.1" /db-xref="GI:21956909" /translation="MDKLKLRQLTGHHEFYLG LLVLLAIGLSVQSPEFLTGLNLT DV ATSYAILGILACGLFVVLIAAGGIDISFPAV TAIA QYVMASWVITQGSFPLALVMAMA VGLLLGLINGLLVYWLKVP AIIITATLNLFYGL LVYFTNGTWLYGFPDWFMTGINWF SFEGSDGYDYLTLPLLC LAGTIIFTGVMMNYTR LGRQIFAMGSNKDAASRLGINIFR LHLYVYGYMGILAGVA AVVQAQISQSVAPNSLMG FELTVLAAVVLGGTSM SGGRGSLT GTVLGVMLLAFLQNG LTLLSVSSYWHTVFS GVII LVSISTTAWNEKRKLL REH"
gene	complement (247372..2488 68)	/locus-tag="y0234"
CDS	complement (247372..2488 68)	/function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="residues 116 to 498 of 498

are 61.19 pct identical to
residues 9 to 392 of 392 from
GenPept :
>gb|AAG54671.1|AE005211-6
(AE005211) putative ATP-binding
component of transport system,
probably ribose specific
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="putative ATP-binding
protein of ABC transporter"
/protein-id="AAM83828.1"
/db-xref="GI:21956910"
/translation="MTQATAFITLENISKRFPGV
LALDGVNLTNLKGEVHCLAGQNGC
GKSTIIKVISGVYQPEKGASILIDGKLLHQLTPQ
LSFYYGVQVIYQDLSLFPNLTVAE
NIAVHRYLPGGDFWVKRKS MRERALAAMQRVGVT
LDLDDKKVEQLSIADRQLVAICRAI
AADARLVIMDEPTASLTSQEVKGLLNVRDLKSQ
GICVVFVSHRLDEVMEVADRISVM
RDGKWVGWQASELDSHELAFMTGQRFTYRPLP
PLAAKAAPLLEIRKLSRGEQFRNI
DLTLHQGEIVSITGLLGAGRTELCLSLFGMTQPE
SGEIFVAGEPVFRHNRDAIRHGI
GYVSEDRLTQGLIMEQSIYDNTIVSVFDQLHTRS
GLLDHSKAAALVNKLVDLNIKVS
DTALPVKTLSGGNAQRIAIKQVATQPRILILDS
PTVGVDIANKEGIYHIAKALAEQG
MAVLMICDEIPEAYYNSHRVLMVRKGELIAEFYP
HQCTEQQIAEVVNG"

gene complement (249072..2501 /locus-tag="y0235"
30)
CDS complement (249072..2501 /locus-tag="y0235"
30)

/function="transport; transport of
small molecules; carbohydrates,
organic acids, alcohols"
/note="residues 25 to 350 of 352
are 53.37 pct identical to
residues 5 to 327 of 328 from
GenPept :
>gb|AAG54669.1|AE005211-4
(AE005211) putative periplasmic
binding protein, probable
substrate ribose [Escherichia coli
O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="putative periplasmic
binding protein of ABC
transporter"
/protein-id="AAM83829.1"
/db-xref="GI:21956911"
/translation="MQHNKISYLATVPLPERKQE
GIAMKFNALLNVCIVSACMLFTT
QTLAAEKKHEIAVVAKVTGIPWFTRMEVGVNEAA
KKLVNAYQVGPATPDPAQQVKVI
EDLIAKNVDIIVVPNDKVLKKAQEKGV
VLTHESPDQRIGQWDVETIDSEKY
AQANMDELAKAMGNKGGYAIYVGS�TVPLHNAWA

		DYAIKYQKEKYPEMFVTPRLPVA ENIDKSYSTTLDLMKTYPQMKGIIGFGLPIGA GQAVAKKRAKDQIAVVGIAMPAQA APYLMRGDIKKALLWDPKDAGFAVVEIANQLLNG QKVTEDLTIDGLGKADVDSKNGVI RFNKILEVTKDNAKTGLF"
gene	250774..251775	/gene="ddg"
		/locus-tag="y0236"
CDS	250774..251775	/gene="ddg"
		/locus-tag="y0236"
		/function="putative factor"
		/note="residues 25 to 333 of 333 are 66.66 pct identical to residues 20 to 327 of 328 from E. coli K12 : B2378; residues 28 to 333 of 333 are 66.66 pct identical to residues 1 to 305 of 306 from GenPept : >emb CAD07638.1 (AL627274) putative acyltransferase [Salmonella enterica subsp. enterica serovar Typhi]"
		/codon-start=1
		/transl-table=11
		/product="putative heat shock protein"
		/protein-id="AAM83830.1"
		/db-xref="GI:21956912"
		/translation="MSEDMYRYRVMSLCVTHSHL THNDRVHMIKPQKFHISLLHPRYW LTWFGLGVLFLLVQLPYPLLNKLGVLGRTSMRF LKRRVSIARRNLELCFPDMDKQVL EQTIIGNFESLGMGLLETGMAFWSDTRIQRWFS VSGLENLKRAQQGKRGVLVIGVHF MSLELGGRVMGQCQPMAMYPHNNKVMELVQTW GRMRSNKAMLDRLRGMVRALKQ GEAVWFAPDQDYGPRGSVFAPLFAVEHAATTSGT FMLARLAKPALLPLVLLRKKEGRG YDLLIQPALEDYPIDDEIAAASYMNKVIEKEIMR APEQYLWLHRRFKTRPIGEPsLY"
gene	251819..253114	/locus-tag="y0237"
CDS	251819..253114	/locus-tag="y0237"
		/note="residues 186 to 247 of 431 are 26.15 pct identical to residues 515 to 579 of 865 from GenPept : >dbj BAB73440.1 (AP003587) ORF-ID:all1741 probable proteinase [Nostoc sp. PCC 7120]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83831.1"
		/db-xref="GI:21956913"
		/translation="MKGKRAVGVGITAHFILWF NRSNVALIPFFEGPSIMKSLILL ALLIPASVTANTLSVEPKDTKPALIDSLSATFAI DKIAMLKKEKGANESNLYLPFEQT KDGLAILFGDINQDGKIDALVPFTWEGLNGLDQE IPSNDWYSYAIYLQDDQGWKQVG QIPTGTFTTDNQTLTNIEDGVIYGEIMPRMTDD DPQPQQWVLRAHPEKDNLLVPIPT PQPLANALTLNLSKKRPLTRNALVTAFGEPINIG"

DNYFLVDGDCVGHDPWKYYQYPGA
AFNVSQNDNSVGVSFIGIPDNLSLVLGDLTITQ
K TSAHQLIKALSQNSFTVSRST
DLRTDLGQSSPYFDDANDIFALRLPYIAGFEAW
AKKNEAREVPNDEEADTFTRQFYF
TTTIGVAPIQNSPTRLMFYFLGDKMVALSVIYDD
GQVCI"

gene complement(253332..2550 /locus-tag="y0238"
02)

CDS complement(253332..2550 /locus-tag="y0238"
02)

/note="residues 8 to 554 of 556
are 75.13 pct identical to
residues 1 to 547 of 549 from E.
coli K12 : B4065; residues 5 to
555 of 556 are 74.95 pct identical
to residues 13 to 563 of 563 from
GenPept : >emb|CAD09253.1|
(AL627282) putative
sodium/hydrogen exchanger family
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83832.1"
/db-xref="GI:21956915"
/translation="MWSLKESMEIFFTILILILV
VSLSGVVTRMLPFQVPLPLMQIVC
GALLAWPNFGLHVNFDPELFLVLFIPPLLFADGW
KTPTREFIHHGREILGLALALVLV
TIVGIGYLIYWMVPGIPLVAAFALAAVLSPTDAV
ALSGIVGKGRIPKSIMGVLEGEAL
MNDASGLVALKFAIAVAMGMTMIFTVSGATLEFLK
VAIGGLLAGVAITWLYSKSLRIMS
RWSGDDPATQIVLLLLLPFASYLVAEHLGVSGIL
AAVAAGMTISQSGIIRNAPLAMRL
RADSVWSMLEFVFNGMVFI LLGLQLPGILETSIT
QAELDPTIQTNL FADV AIIYGAL
LLLRFGLWLSMKKISKRVLTKRPLQFSDYTTREL
WVASFAGVRGAITLAGVLSIPLFL
SDGSAPFSRYQLVFIATGVILLSVIIGVIALPPL
LRGVVADKSASREEIRLARAAMA
EVAIVSLNKMEERLMTSSEENIDSELLKEVSSRV
IGTLRRRTGSKDEVENTLLIENLE
RRFRLTALRAERGELYHLRATQKISNETLQKLLH
DLDLLEALLIEKEG"

gene complement(255330..2566 /locus-tag="y0239"
85)

CDS complement(255330..2566 /locus-tag="y0239"
85)

/note="residues 4 to 451 of 451
are 85.04 pct identical to
residues 2 to 449 of 449 from E.
coli K12 : B4064; residues 9 to
451 of 451 are 87.35 pct identical
to residues 13 to 455 of 455 from
GenPept :
>gb|AAG58013.1|AE005518-7
(AE005518) Z4223 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1

		/transl-table=11 /product="putative transporter" /protein-id="AAM83833.1" /db-xref="GI:21956916" /translation="MSSSNPQAQPKGTLDAFFKL SERGSNVRQEVLAGLTTFLAMVYS VIVVPSMLGKAGFPPTAVFVATCLVAGLGSLLMG LWANLPMaIGCAISLTAFTAFSLV LGQQISIPVALGAVFLMGVLFTHSVTGIRSWIL RNLPMGVAHGTGIGIGLFLLLIAA NGVGLVIKNPIEGLPVALGAFTSFPVIMTLLGLA VIFGLEKLRVPGGILLVIVAISVI GLIFDPSVTYQGLFAMP SLADANGDSLIFSLDIM GALQPVVLP SVLALVMTAVFDATG TIRAVAGQANLLDKDQIISGGKALT TDSVSSIF AGLVGAAPAAVYIESAAGTAAGGK TGLTATVVGILFLLILFLSPLSYLVPAYATAPAL MYVGLLMLS NVSKLDFEDFVDAMS GLLCAVFIVLTCNIVTGIMLGFSSLVIGRVCSGE WRKLVGTVIIAVALVAFYAGGWA I"
gene	257139..257342	/locus-tag="y0240"
CDS	257139..257342	/locus-tag="y0240" /note="residues 7 to 66 of 67 are 38.33 pct identical to residues 26 to 85 of 86 from GenPept : >gb AAG54551.1 AE005201-4 (AE005201) damage-inducible protein J [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative DNA-damage inducible protein" /protein-id="AAM83834.1" /db-xref="GI:21956917" /translation="MANAKALGLDLSTVIRMVVN RLAVNAELPIDLLQPNQETLQAIR DLENGVEVYRVDSVDALKRDLGW"
gene	257698..257781	/locus-tag="y0241"
CDS	257698..257781	/locus-tag="y0241" /note="residues 2 to 27 of 27 are 57.69 pct identical to residues 73 to 98 of 98 from GenPept : >gb AAF96231.1 (AE004370) conserved hypothetical protein [Vibrio cholerae]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83835.1" /db-xref="GI:21956918" /translation="MPDLLLIYQRTDSEIKLYRV GSHSDF"
gene	complement (257961..258815)	/gene="ssuB"
CDS	complement (257961..258815)	/locus-tag="y0242" /gene="ssuB" /locus-tag="y0242" /function="transport of small molecules; carbohydrates, organic acids, alcohols"

```

/Note="residues 22 to 256 of 284
are 72.34 pct identical to
residues 8 to 242 of 255 from E.
coli K12 : B0933; residues 16 to
260 of 284 are 72.24 pct identical
to residues 11 to 255 of 274 from
GenPept :
>gb|AAG06830.1|AE004765-3
(AE004765) probable ATP-binding
component of ABC transporter
[Pseudomonas aeruginosa]"
/codon-start=1
/transl-table=11
/product="putative ATP-binding
component of a transport system of
aliphatic sulfonates ABC
transporter"
/protein-id="AAM83836.1"
/db-xref="GI:21956919"
/translation="MASGLSTKIRRSAMTTLTHI
PQGTPTITLESIGKRYGNRTVLDNL
QLRITAGQFVAVVGRSGCGKSTLLRLLAGLEAAS
DGTLLSGNALLSHAKDETRLMFQE
ARLLPWKKVIDNVGLGLRGHWRDEALQVLDTVGL
ADRANEWPAALSGGQKQORVALARA
LIHRPRLLLLDEPLGALDALTRIEMQGLIERLWQ
QHGFVTVLLVTHDVSEAIADRVL
LIEEGRIGLDLAIDLPRPRRKGSAKLAALAEVL
ERVLSPPGIEASRQGIKASRQGT ATSRRVAN"
gene      complement(258773..2595 /gene="ssuC"
70)

/locus-tag="y0243"
CDS      complement(258773..2595 /gene="ssuC"
70)

/locus-tag="y0243"
/function="transport of small
molecules; carbohydrates, organic
acids, alcohols"
/Note="residues 1 to 260 of 265
are 79.61 pct identical to
residues 15 to 274 of 278 from E.
coli K12 : B0934; residues 2 to
264 of 265 are 80.98 pct identical
to residues 1 to 262 of 262 from
GenPept :
>gb|AAG06831.1|AE004765-4
(AE004765) probable permease of
ABC transporter [Pseudomonas
aeruginosa]"
/codon-start=1
/transl-table=11
/product="putative transport
system permease protein of
aliphatic sulfonates ABC
transporter"
/protein-id="AAM83837.1"
/db-xref="GI:21956920"
/translation="MMTISAQRILHRLAPWILPV
ALVVGWQVAVEAGWLSNRILPAPS
AVVTAFWALTKSGELWQHLLTISSWRALIGFSIGG
SIGLVLGVIITGLSRWGERLLNSSV
QMIRNVPHLALIPLVILWFGIDESAKIFLVALGT

```

```

LFPIYLNTYHGIKNIDSGLLEMAR
SYGLSGFRLLTQVVLPGALPSIMVGVRFALGFMW
LTLIVAETISANSIGIGYLAMNARE
FLQTDVVVVAIVLYALLGKLADGSAQLLERVWLR
WHPAYQQKSGEAQ"
gene      complement(259579..2607 /locus-tag="y0244"
27)
CDS       complement(259579..2607 /locus-tag="y0244"
27)

/Note="residues 1 to 382 of 382
are 78.79 pct identical to
residues 1 to 381 of 381 from E.
coli K12 : B0935; residues 1 to
382 of 382 are 81.93 pct identical
to residues 1 to 382 of 382 from
GenPept :
>gb|AAF81710.1|AF250869-2
(AF250869) sulfonate monooxygenase
[Buttiauxella sp. PNBS]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM83838.1"
/db-xref="GI:21956921"
/translation="MSINVFWFLPTHGDGHYLGS
SEGARAVDYSYLQQIAQAADRLGF
GGVLIPTGRSCEDSWLVAASLIPVTQRLKFLVAL
RPGIISPTLAARQAATLDRLSNGR
ALFNLVTGGDPEELAAEGLHLNHTERYEASAEFT
HVWRKVLEGETVDFAGKHIQVKGA
KLLFPPVQHPRPPLYFGGSSAAQDLAAEQVELY
LTWGEPPEQVKEKIEEVRAKAAAK
GRTVRFGIRLHVIVRETTEEAWRAANRLIANLDD
KTIADAQQAFAGFDSVGQQRMAAL
HGGKKDNLEISPNIWAGVGLVRGGAGTALVGDP
TVAQRIQEYADLGIDTFVFSGYPH
LEEAYRVSELLFPHLDLATELPTQRPATQPQGE
VVANIYVPQKVSQS"
gene      complement(260746..2618 /gene="ssuA"
82)
CDS       complement(260746..2618 /gene="ssuA"
82)

/locus-tag="y0245"
/function="transport of small
molecules; carbohydrates, organic
acids, alcohols"
/Note="residues 18 to 333 of 378
are 73.10 pct identical to
residues 17 to 331 of 333 from E.
coli K12 : B0936; residues 18 to
333 of 378 are 73.41 pct identical
to residues 17 to 331 of 333 from
GenPept :
>gb|AAG55421.1|AE005283-8
(AE005283) orf, hypothetical
protein [Escherichia coli O157:H7
EDL933]"
/codon-start=1
/transl-table=11
/product="solute-binding
periplasmic protein of aliphatic

```

		<p>sulfonates, ABC transporter" /protein-id="AAM83839.1" /db-xref="GI:21956922" /translation="MSLSFFFRRGFNVHRLNIG AMAAIITLAFTNTVIAQDNAPQF RIGYQKGSVNLVLAKTHQLLEKRF PDTQISWIEF PAGPQMLEALNVNSIDLGSTGDIP PIFAQAAGADLLYVGMEPPKPKAEVILVPENSAI NSVAELKGHKVAFQKGSSSHNLLL QALQKAGLKFTDIQPVYLTPADARAAFQQGNVDA WVIWDPYISAALLQGGIRVLIDGS QLNQTG SFYLASRPYTEANGPFIQQVLEVL TQAD ALTLS DRAQSITLLANAMGLPEAV IASYLDHRPPTAIQPLSQATVAAQQRTADLFFAN RLLPVKVDISQRVWQPAGQLSSKP PSSKPSSSKPSSSNQSSPSQLPTDQPSIAQTSIE QSSTAKSQTK"</p>
gene	complement(261897..262478)	/locus-tag="y0246"
CDS	complement(261897..262478)	/locus-tag="y0246"
		<p>/note="residues 1 to 175 of 193 are 61.14 pct identical to residues 1 to 175 of 191 from E. coli K12 : B0937; residues 1 to 175 of 193 are 61.71 pct identical to residues 1 to 175 of 191 from GenPept : >dbj BAB34443.1 (AP002553) NAD(P)H-dependent FMN reductase [Escherichia coli O157:H7]"</p> <p>/codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83840.1" /db-xref="GI:21956923" /translation="MRVISLAGSPRTPSRSAALL NLSQHWLQQQNVEVIPYTLHDFQA DDL L RANFNSPDVSAFVAQLATADGLLIATPIYK ASFSGALKTLLDLLPERALDHKVV LPLATGGSIGHMLAVDYALKPVL TALKAQEVLHG VFVDDSQVVFHGEQVTVSTSATTR LEEALSFY LALGRRKPLASNAVSSSLVQQTA A"</p>
gene	262949..263650	/locus-tag="y0247"
CDS	262949..263650	/locus-tag="y0247"
		<p>/function="enzyme" /note="residues 9 to 225 of 233 are 34.10 pct identical to residues 11 to 222 of 224 from GenPept : >gb AAB85318.1 (AE000859) deoxyribose-phosphate aldolase [Methanothermobacter thermautotrophicus]"</p> <p>/codon-start=1 /transl-table=11 /product="putative deoxyribose-phosphate aldolase" /protein-id="AAM83841.1" /db-xref="GI:21956924" /translation="MIDFNDPRQVAKAIQFTNVN ADLTREGVIKHLNICLEYQFDAAM IAPCWVYLAKDVLKSGSVRVATTNVNFPQANDTTA</p>

gene	263804..264736	MKVAIVRELAKEGADEFDFPPNPG FLLGGLDELYFNELKEVTHIAHDLGMKVKAMLEF GFITEEAMKIKATRYAYEAGIDWV KQSSGWGKGGCAATVEDVQLLKANIQAPCRVKVS GKVNTLEKMKEMFLAGAELVGTSS GPELVKGLTGDINAY"
CDS	263804..264736	/locus-tag="y0248" /locus-tag="y0248" /function="enzyme; degradation of small molecules; Carbon compounds" /note="residues 4 to 299 of 310 are 39.26 pct identical to residues 5 to 301 of 308 from GenPept : >gb AAG05338.1 AE004621-9 (AE004621) ribokinase [Pseudomonas aeruginosa]" /codon-start=1 /transl-table=11 /product="putative ribokinase" /protein-id="AAM83842.1" /db-xref="GI:21956926" /translation="MMSVFILGSYAKALVMTTDR IPLAGETLIGYDFRQTWGGKGSMD AVQAVRLGAEVAYAGVVGDDTFGHEFVGLMQEEG VNIDALTISGELPTGAGLIVKDKE ARNVIVVDMGANKLFTPALVDSALSQKQSNVVL TQLEIPLETARYGLQRAKEFGKIT ILNPAPARDLRLDLISAIDYLTNPNETEARVALGL PPDDPRSNREIANLLELTGCQYVV MTLGESGSAVFGRNDTQEIPPCIIDVDSNGAGD SFNAALAVALDEGLPISEAVLFAN ATAALCCMDWETVPSYRYREDVDAFMRSITVKEE " /locus-tag="y0249" /locus-tag="y0249" /function="putative transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="residues 1 to 135 of 167 are 34.04 pct identical to residues 1 to 139 of 139 from GenPept : >gb AAC22159.1 (U32732) high affinity ribose transport protein (rbsD) [Haemophilus influenzae Rd]" /codon-start=1 /transl-table=11 /product="putative inner membrane permease" /protein-id="AAM83843.1" /db-xref="GI:21956927" /translation="MRPDRILHPELAAALATLGH TDIILVTDAGFPIPPQAKRIDLGF WPGTVDVLHILRVLKKEIFVEEVRFASEVRDCHP QLYRDVQTLTYTGSGAEFQAASHET LCHDLAHQAKVVIRSGSFNPWANFALVASTDPFA WFTDESGVKPLPAYVARRQRILDN VVPELNA"
gene	264742..265245	/locus-tag="y0249"
CDS	264742..265245	/locus-tag="y0249" /function="putative transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="residues 1 to 135 of 167 are 34.04 pct identical to residues 1 to 139 of 139 from GenPept : >gb AAC22159.1 (U32732) high affinity ribose transport protein (rbsD) [Haemophilus influenzae Rd]" /codon-start=1 /transl-table=11 /product="putative inner membrane permease" /protein-id="AAM83843.1" /db-xref="GI:21956927" /translation="MRPDRILHPELAAALATLGH TDIILVTDAGFPIPPQAKRIDLGF WPGTVDVLHILRVLKKEIFVEEVRFASEVRDCHP QLYRDVQTLTYTGSGAEFQAASHET LCHDLAHQAKVVIRSGSFNPWANFALVASTDPFA WFTDESGVKPLPAYVARRQRILDN VVPELNA"
gene	complement(265407..2663 48)	/locus-tag="y0250"
CDS	complement(265407..2663	/locus-tag="y0250"

48)

		<pre>/function="regulator" /Note="residues 54 to 306 of 313 are 23.57 pct identical to residues 51 to 302 of 307 from GenPept : >gb AAG06959.1 AE004778-3 (AE004778) transcriptional regulator MmsR [Pseudomonas aeruginosa]" /codon-start=1 /transl-table=11 /product="putative AraC-like regulator" /protein-id="AAM83844.1" /db-xref="GI:21956928" /translation="MACHDEPGYSLNFCQHRVG RMEKNMQRTQVVANWYRESDEFST LVNYRILRAGHIRAADNFHVRQSVAGHELIFCL NGSGFIRLENNLHEVKKGNLAWLP VRWPHEHFPNKQEPWEILWLRIDGAKLNNIMQIL DVAQQPVFEFTSPETITDIYHRLF DLMQSHTLVADAHCDVLCSQLIYTLLNRSFDT KSPVISHRGLGRLIYQIHSYND WDIDKFMQYCQVSKSQLFRLFQETFNQSPLRWLK NYRLSQARRLLVETEETISRIAGL VGYNDPLHFSRDFHRSVGLSPSDFRRQERQLDND RHD" /locus-tag="y0251" /locus-tag="y0251" /Note="residues 18 to 370 of 376 are 43.94 pct identical to residues 13 to 359 of 362 from GenPept : >dbj BAB49039.1 (AP002998) hypothetical protein [Mesorhizobium loti]" /codon-start=1 /transl-table=11 /product="putative oxidoreductase" /protein-id="AAM83845.1" /db-xref="GI:21956929" /translation="MDTLISQLEHATQPVLPKRR DYRIGIIGAGFIVEHCHLVAYQKA GFVPYGITSKEHSQNHRLAETFAIKKVYETWQDM VCDPQIDIIDIAPVPHIQLEIVRF ICESNSAAKHIGILCQKPLAMSLKDGREIVRLS QQSGIPIAVNSNMRYDPSMRALKY ILENQLIGDPVIASIDMRAIPDWQAFQKYKKLE LYAMAIHHIDAFRFLFGDPVKVTA VCRTDPRTTTEHIDGITQYTFQYANGLIATSLDD VWAWPGEPKANNYINWRVEGSDG LAEGDFGWHRRPEYCGSTLKLASRNHPGQWIAP KWERQWFPDAFIGTMANLMCAIEE NRPPEISAEDNLGTLACIEACYLSIQQERTVYLN EILLENAK" /locus-tag="y0252" /locus-tag="y0252" /Note="endonuclease motif; residues 1 to 298 of 299 are 51.48 pct identical to residues 1 to 303 of 304 from GenPept : >dbj BAB49038.1 (AP002998)</pre>
gene	266543..267673	
CDS	266543..267673	
gene	267670..268569	
CDS	267670..268569	

		unknown protein [Mesorhizobium loti]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83846.1"
		/db-xref="GI:21956930"
		/translation="MINVGIFTGYYPYTLSGTID KIKQAGMGCVQLDLEFTDIDLRRG RITKEKAHQVRNAFRANIPIVASAYTNLVHPD PVKRAENIAAVKEILAHARHFGTP YVISEGTGTYNTSDWLYDPKNSTEEAYQEFKAIA KELATFAYEHNAVFLVENYVNNII GSVGQVARLMQVEVHPGLGLALDPTNYFDDKNID AIDETLHNIFNVLESRIKIAHAKD CKKTDAIAEKFGGGA AEHNSFRGAGSVELPAAGL GALNYPLYVELLAQKHPNIPLIIE HVDEEDIPRAKRFVDEVLMATGS"
gene	268784..268858	/locus-tag="y0253"
CDS	268784..268858	/locus-tag="y0253"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83847.1"
		/db-xref="GI:21956931"
		/translation="MDWIQDNSEMYLAGDWLTQT GLTG"
gene	complement(268916..269710)	/locus-tag="y0254"
CDS	complement(268916..269710)	/locus-tag="y0254"
		/note="residues 42 to 145 of 264 are 31.77 pct identical to residues 163 to 258 of 325 from GenPept : >emb CAB12673.1 (Z99108) similar to iron(III) dicitrate transport permease [Bacillus subtilis]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83848.1"
		/db-xref="GI:21956932"
		/translation="MCTAIAIYG TENIPPETAYE IGMLFFKVIELDITSTGYKYRED RSEEDIDFIEVSLSDLKNELKNKNATSFRFYNES EKSNYWTASFGFSTSDFGGFYHFD AQCALSKNGKEKFIEFIKEFSKNNFSYGIVYNP DNVADGFYYAEGGNFVQIYQYENP MFFEKETGGMYEGQERYKNTMLRMVYPVNVINHH HLDIIIGNVSLKEWISSDEKHGTL EGLNNDLWLWTVEDTKLDEVNKYLGEAGVLISWK PPTIKKAPRKLP"
gene	complement(269719..274263)	/locus-tag="y0255"
CDS	complement(269719..274263)	/locus-tag="y0255"
		/note="Rhs element associated; residues 89 to 1396 of 1514 are 33.53 pct identical to residues 112 to 1362 of 1517 from GenPept : >emb CAD18288.1 (AL646083)"

putative RHS-related transmembrane
 protein [Ralstonia solanacearum]"
 /codon-start=1
 /transl-table=11
 /product="Rhs-like core protein"
 /protein-id="AAM83849.1"
 /db-xref="GI:21956933"
 /translation="MFMTVAQSIGTGYGAAGAQ
 ALRQTALGQQSPARTDYQVSNPNV
 GNIARASDSSLNVAESQQFNTLVTAGFGMQAIAA
 GVAGGYVGAKIGNKLGHGIARALN
 FNQVATEGESPAHLGHPIAHQKKDWGVWGAIGGI
 LLGAAAAALVVVTFGTGLVVIAAA
 AAAAGLIGGIAAATGAALGQYGDNKGVIAGSAN
 VFFEGQPVARVGDKIQCSDHPSSP
 PPMIAEGAKTVFANQKQIARLGHRTTCDGNINAG
 CGSLAITQETAYVYEVADSRNPYL
 RWSAVILSFLPIQKKFEQGFRLKKPPNTAVNAT
 HNCPTGSDPDMVSGDYLQVWPVI
 DIAGVLPVRLQRTYRSGDYFTVSGCFGHKWADSW
 SQHLVVHEDNIDYIDEEGVGLSFF
 TPENKVQAVNLNRLRYELVGERHGELRVFDRSTQ
 QTLHFNQQQQQRYLSAITDRKGN
 RIDFRYQQGELISVEHSDGYVLEIDSRGRTIHAV
 ELVTQEKRQKLLQSTFSERGYLVQ
 CQSFQYGTLSHEYDPKGYMVRWRDSTDVAVRY
 DISGRVVALKTSTGFFADHFIYHD
 KERYTIYRDGEGGETGYHYNENLLIKLVDPLGN
 TTLTDWDLTQKIKETDALGRITRF
 IYNERGDLTAVILPDETRTEYEYNPSGVVTAFTS
 SAGDSWQYQYDRQGLLRQVTYPSG
 QTMSFRYGKKGEVLRKIIAEDQVWRYHYDHHGCL
 STIIDPKGNSTAVTLDVLGRLFSH
 QNALGELTRYTHSDAHASPAGSVTKMVMPDGVEQ
 AIAYDSEKRIAAALTDGAGKTTRYE
 YGGFDLLTGLIRPDGQRLTFGYDTLTRLNQVTNA
 SGDTYRYTRDRAGQVISETDFGTGR
 TVHYQYDAVGRRIGARYPDQRLVRWHYSMDQVL
 AQQTWHCDALSSTLVGTVSYGYDG
 AGRLLSATNADAVVEFDYDEAGQLVAERLNGREV
 RHQWDALNGTPVARQVGELGLTFV
 YGAQGELTRLQLAGHQPLQLQHDRLGRETVRESA
 AGFIQACNYTPSGLLAHQAGRNS
 ALFQQQLIAPESPALHGSAVNRSWQYDRAYNVVG
 MDDGRWGKTQYQYDRNDQVVRADF
 GGFLPLQEQFSYDVNQNLREHRCLPRGAQAVLAQ
 ASQQQQAGRVVVKRGDSQYRYDAAG
 RLVEKRSQKDGYPQLWRYRWNEQDQLSELITPT
 GARWRYGYDAFGRRIRKLRVVDTP
 PLNEMDAPSTGPATASLAGYAYLWSGDQLIEEVP
 VYADGTVAYEQGIHWLYAPGGLTP
 MARYAQGKLHYVVADHLGTPRELLNEQGKVVWAS
 RLSTWGQAEWLRQAANEEDRVSCN
 LRFAGQYADAESGLHYNRFRYYDGETGQYLCPPD
 IGLEGLNPYGYVHNPVSWVDPLG
 LATCPMREVNNGTKIFGKGQKDGTPGHDQFSEVIA
 NKLAMSGKFKEVYLNRSYNFANGK
 GISGRRPDIMAVDMNGKVHAIELAS
 KTDMDGRKFPSLRTRNQDAMKNLPSIDRGSVIVL
 EHQYNSSKIKNALDNLISGI"

gene

complement(274302..2747 /locus-tag="y0256"
 24)

CDS	complement(274302..274724) /locus-tag="y0256"	/note="residues 1 to 137 of 140 are 36.49 pct identical to residues 4 to 140 of 143 from GenPept : >emb CAD18289.1 (AL646083) conserved hypothetical protein [Ralstonia solanacearum]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83850.1" /db-xref="GI:21956934" /translation="MYYFNEGSLELPEAWRDMTV NVLTSSLDETIVGLSFTVSRDTPPW GMGFHEFFDREIGSLSRQLNHYQLLHQDTGEVNN HPSVTAEFCWSSEQGRIHQMLTLV DIAPRVLILTATMVGELTPQQKEHITAIVQTLQI NARS"
gene	complement(274727..276829) /locus-tag="y0257"	
CDS	complement(274727..276829) /locus-tag="y0257"	/note="Rhs element associated; residues 77 to 696 of 700 are 46.91 pct identical to residues 3 to 633 of 633 from GenPept : >gb AAG54902.1 AE005236-3 (AE005236) Z0707 gene product [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="VgrG-like protein" /protein-id="AAM83851.1" /db-xref="GI:21956935" /translation="MSGAQMTEMAGGIGDAVGGT AGKRINQAAEVAKTALDAKAKVLD GGVTPLNLAAGGAGAGLPDSAAAALTRLVKQPSG LQFTLTITASLPPQTFVAVDFTLSE MLSSPFVLNVGLASADPAVDFAAVLDEDATLFIW REGVLQRSITGMVASFEQGDGTGFH QTRYSMVIRPALWRTSLRRNARIFQQASVEEIIIT TLLKENGINDFAFGFRHPHPVREF CVQYQESDFDFIQRLTAEEGIFYFFESAGKNTV VYADDVGS LPKGASLPYNPNVAAQ AQELSITTFTRSAQVRPAMVQLKDYTFKNPNWAA AFSEQSGELQNQRPDYEHFDFPGR FKDAQHGQDFTRYRLDALRNDANLGQGASNDFTL QPGQLFSLYNHPRGDLNHAWQLLG VQHSQKMQALEQASGDQGTVLFNHFSFIPHTQT WRPTPLAKPAMDGPQIAMVVGPPG EEIYCDEYGRIRLQFLWDRYGQSDNNSCWIRVT QPWAGQGWMGLAIPRIGQEVVVDF LHGDPDQPIVTGRTYHANNIPPGSLPASKTQMAF RSKTHQGEQYNEMRFEDAKGGEGL FMHAQKDMSTTVKDNQTTTVEKGNQTVTVEKGDR TVTVATGNETTDITQGSLETETIKV RRSTCANFIQVKAEGDAPGTQLYTATEQIKFVVG KSSITLNPDSIILQFSGSTSITLN AANIDAIAPLINLNKDKG"
gene	complement(276826..276924) /locus-tag="y0258"	

CDS	complement(276826..276924)	/locus-tag="y0258" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83852.1" /db-xref="GI:21956936" /translation="MFAHDKANNKKTADKTGTVT PTHIVSPEAAQP"
gene	complement(276946..277122)	/locus-tag="y0259"
CDS	complement(276946..277122)	/locus-tag="y0259" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83853.1" /db-xref="GI:21956937" /translation="MQTELNREIPLEELLRQLAV SADEHQPASPVLIKQIDDRWNALL SRYHHLTQQTNSAR"
gene	277204..277692	/locus-tag="y0260"
CDS	277204..277692	/locus-tag="y0260" /function="regulator" /note="residues 48 to 154 of 162 are 33.64 pct identical to residues 6 to 108 of 112 from GenPept : >gb AAF94621.1 (AE004224) transcriptional repressor RstR [Vibrio cholerae]" /codon-start=1 /transl-table=11 /product="transcriptional repressor" /protein-id="AAM83854.1" /db-xref="GI:21956939" /translation="MHRITISNSIAIRCVFVFKS GLILEHLMTDVIDEIMQTEEQRA FGLRLKELRKQQHKTQKEVATRIGLQLSQYNKYE SGMHIPPADKLITLAELLVTSIDY LLLGSSNETSSIRNTRLLERFKALSQCQPEEQET VIKLIDAVIVKHRVESALQPVDPE KK"
gene	277774..277998	/locus-tag="y0261"
CDS	277774..277998	/locus-tag="y0261" /note="residues 15 to 68 of 74 are 42.59 pct identical to residues 35 to 88 of 132 from GenPept : >gb AAA97244.1 (U14003) ORF-f132 [Escherichia coli]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83855.1" /db-xref="GI:21956940" /translation="MAKAHSTSGTGINKTPKTER YYTVGYVPQRGKRNPFPAINLKGR WLEALGFFSGQPVLITVEHGRLVIQPEIKI"
gene	complement(277977..278174)	/locus-tag="y0262"
CDS	complement(277977..278174)	/locus-tag="y0262" /codon-start=1

		/transl-table=11 /product="hypothetical" /protein-id="AAM83856.1" /db-xref="GI:21956941" /translation="MSHSPDRDSSPLSCIQAITI LLYFKYCAGRKSCINNIGFVDNEF RDIIVHNTVENNIPIHIFISG" /locus-tag="y0263" /locus-tag="y0263" /note="residues 15 to 63 of 63 are 34.69 pct identical to residues 177 to 224 of 243 from GenPept : >gb AAG55242.1 AE005267-7 (AE005267) arginine 3rd transport system periplasmic binding protein [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83857.1" /db-xref="GI:21956942" /translation="MQDLRPAQYLKYNNIVMAWI QDNGELSLSGEWLTQTGLTGQPLA ISVMAGKVIIQFQKMNMLL" /locus-tag="y0264"
gene	278074..278265	
CDS	278074..278265	
		/note="residues 17 to 157 of 161 are 25.97 pct identical to residues 29 to 169 of 192 from GenPept : >gb AAC12984.1 (AF020713) unknown [Bacteriophage SPBc2]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83858.1" /db-xref="GI:21956943" /translation="MKNPCQNCEKNIDLSDIKSV EKTILGYSFPEAFVSHYLSFNGGVP LRAWWACDDGCEPLEIAAFKPFKYHKMTNDNPNS LIDGCYNEMIRKNVIPSNIIPFGN DWGGNFFCLNKDDSVVFYATDSFDPEVSMKSNH DVLQKKLTSSFEEFINGLVEEDDL E" /locus-tag="y0265"
gene	complement(278315..278800)	
CDS	complement(278315..278800)	
		/note="Rhs element associated; residues 8 to 326 of 456 are 44.23 pct identical to residues 957 to 1250 of 1354 from GenPept : >emb CAD08751.1 (AL627266) Rhs-family protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="rhsD protein" /protein-id="AAM83859.1" /db-xref="GI:21956944"
gene	complement(278802..280172)	
CDS	complement(278802..280172)	

```

/translation="MAADLLPRQGDIWRKFSFDT
AGELSMATDFIRGEQQYRYDAEGR
LTDSRERHQLSVAEDFAYDNADNLLNLRKLPFDT
VDPLYDTPVANNRLTQWQHRYFEY
DAWGNMTTRHAGGRMQHFAYDDNRLLRWGTGP
LGEHDSHYRYDALGRRIHKSVTIK
RGAECTTRQTDFIWQGLRLLQEQTGDNATYIYD
PNESYTPLARVDQRHGETESQVYY
FHTDINGTPLDVTGEGKHRWSGKYHAWGKVTRQ
NVSDPRQSTVSRFAQPLRYPGQYS
DDETGLHYNTFRYYDPEIGRFSTQDP IGLAGGIN
LYQYGNPLTWIDPWGWAFFGGVDF
TGSPDLFPVKGSQNLNIVEITMQGARGRDFTEAFK
LAGISKADATGYTWHHLNDFDPVS
GKTTMQLVTTSAHEATFPHAGSVSQFEKHFNLP
QSYGSADAVAISHSKGWLKGRIPK ALRSGC"
gene      complement(280200..2830 /locus-tag="y0266"
91)
CDS       complement(280200..2830 /locus-tag="y0266"
91)

/note="Rhs element associated;
residues 10 to 960 of 963 are
37.73 pct identical to residues 1
to 934 of 1364 from GenPept :
>gb|AAL19248.1| (AE008708)
putative RHS-family protein
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="Rhs-like protein"
/protein-id="AAM83860.1"
/db-xref="GI:21956945"
/translation="MRRGPGRPAMFEARVDDKL
YHSSALAGFIIGSIIGAIVIFAAA
AYAASIVLTGGATLVATGFIVGMGVTTLGVVAGG
LIRSVGEKIGSMCHHDVQGITTGS
KNVKVNSKRAAHVELSTVACKDDSAIQMAEGSS
NIFINSKAAVRLEDKTTCDVVDS
ASSNVTFGGGRVQYLDIKREISDEMRDLSEKLF I
VAGLAGGIFGAAKQAGCFGLKCLS
KIALGEMAGAAAGYGLEKGVGAIAGYFGYPVDVI
SGQKLLTGEGDDTDFILPGIFPLH
WSRIYRSENHHVGALQGWSLVWERSLRKEDDS I
VYQNDEGREIVFPLIKRGERYFSP
TEHIWLARTERDTYAISSPFETCFIFEAFSEAGV
AKLASLEDLNGHALYFSYDDIGQL
KKISTTSGYGVYCQYEKGRVSVACVKGGTPGTL
VRYQYNEQHQLVSVTNREGQITRQ
FGYHGHLINKLADVRLGECRYTWADIGGTPRITH
SATNLGEQWQFDYDIDNQQTTLTD
LNTGQTACWGYNAQHLITDYRDFDGGKYAFDYND
LNMPVRVVLGERTLVLVYDALAR
PIQITDPLKRETHIDYHRNSLRVRRQYPDGQVW
KGEYDRTGRLLKENAPDGGVTLYH
YPGASSLPERITNAVGAQTHLGWERHGQLTEHTD
CSGKLTRYEYDIDGHLLTVIDAEN
HSTHYSYNRLGQPTGIRYADGRKEQLRYNAQGLV
EQFTDPVGRQLHWRYNLRGQPVSF
TDRLQREYRYRYDCHGQMIELDNANGGQYHFRWS
SGGQLVEEQYPDNLVRRYRYGESG
MLMALETTAPTVDLTVSRQVSFDYDAGGRMTQR
LTGMSATRYDWDIMDRLLLAERP

```

		TAVGEQAGIVGHGVRLAYDKAGHLLTESGDLGAV TYQWDPLHHLAALTLPDGQTLISWL RYGAGHVSAIRHGDTLISEFSRDNLHREVSRTQG ILTQYRDYDAMGRRL"
gene	complement(283057..283515)	/locus-tag="y0267"
CDS	complement(283057..283515)	/locus-tag="y0267"
		/note="residues 9 to 144 of 152 are 35.71 pct identical to residues 5 to 144 of 148 from GenPept : >gb AAL19247.1 (AE008708) putative cytoplasmic protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83861.1" /db-xref="GI:21956946" /translation="MPENNINTYCIQEGTLECPE GFTDRTVNLFMKGKPGAAFALNIA RDVPEAHEVLSDYVQRQIGILKDNLKKYEVKKHQ QIDVGAQHIPGEYVEATYMAETRR VWQRQVAIQVGDHMMIFTATNASPFNPQQQATWE QWIHSFAPWAREAGHV"
gene	complement(283521..285923)	/locus-tag="y0268"
CDS	complement(283521..285923)	/locus-tag="y0268"
		/note="VgrG-like protein (Rhs element associated); residues 169 to 792 of 800 are 44.06 pct identical to residues 3 to 674 of 713 from GenPept : >gb AAC62387.1 (AF044506) VgrG protein [Escherichia coli]" /codon-start=1 /transl-table=11 /product="VgrG-like protein" /protein-id="AAM83862.1" /db-xref="GI:21956947" /translation="MFAHDKANNKKAADKTGTVT PTHIVSPEAAPTIVSGAQMTEMAGG IGDAVGGTAGKRINQAAEVAKTALDAKAKVLDGG VTPTNIVATGPAPTIVSGAQMTEMA GGIGDAVGGTAGKRINQAAEVAKTALEAKAKVLD GGVTPMNLAAAGGAGAGLPDSAAAA ISRLVKQPSGLQFTLTASLPPQTFAVVDFTLSE MLSSPFVLNVGLASADPAVDFAAV LDEDATLFIWREGVLQRSITGMVASFEQGDGTGFH QTRYSMVIRPALWRTSLRRNARIF QQASVEEIIITLLKENGINDFAFGFRHPHPVREF CVQYQESDFDFIQRLTAEEGIFY FEFSAGKNTVVYADDVGS LPKGASLPYNPNVAAQ AQELSITTFTRSAQVRPAMVQLKD YTFKPNPWAAAFSEQSGELQNQRPDYEHFDFPGR FKDAQHGQDFTRYRLDALRNDANL GQGASNDFTLQPGQLFSLYNHPRGDLNHAWQLLG IQHSGKQMQALEQASGDQGTVLFN HFSFIPHTQTRPTPLAKPAMDGPQIAMVVGPPG EEIYCDEYGRIRLQFLWDRYGQSN"

		DNSSCWIRVTQPWAGQGWMGLAIPRIGQEVVVDF LHGDPDQPIVTGRTHANNIPPGS LPASKTQMAFRSKTHKGEGYNEMRFEDAKGGEGL FMHAQKDMTTMVLNDRKTDVTQDH SEHIGQDQSVTVVRNQSNTIQNDRRVEVTRDQQT EVGNDYQLVVKGEKKEFVTKIRYT EVHEDETLTVTKSIKIHAKQGDISTPNAGITI THDGAIVLQGKYIRLAADMIDLNP EE"
gene	complement (285945..287257)	/locus-tag="y0269"
		/note="disrupted by frameshift"
		/pseudo
gene	287229..287591	/locus-tag="y0270"
CDS	287229..287591	/locus-tag="y0270"
		/note="residues 19 to 79 of 120 are 34.84 pct identical to residues 53 to 114 of 311 from GenPept : >gb AAC17095.1 (AC004482) hypothetical protein [Arabidopsis thaliana]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83863.1"
		/db-xref="GI:21956948"
		/translation="MMICCGVSLMQTHPLIVFLP PKQQEDVMTTINTICLNASVSMRS VSIQSCVSIQSVWQTEFTEQTAREWVVGFIN KDAVRHLAAINLEADIEGVGAHIGQFT GVDQPQLRPRTAEAEGAR"
gene	complement (287382..290842)	/locus-tag="y0271"
		/note="disrupted by frameshift"
		/pseudo
gene	complement (290946..292352)	/locus-tag="y0272"
CDS	complement (290946..292352)	/locus-tag="y0272"
		/note="residues 213 to 462 of 468 are 53.33 pct identical to residues 8 to 259 of 264 from GenPept : >gb AAG54520.1 AE005198-1 (AE005198) Z0251 gene product [Escherichia coli O157:H7 EDL933]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83864.1"
		/db-xref="GI:21956950"
		/translation="MSLVRHMDITSQHPWHVLLQ APLSPEQTAQALADDDPQWEYIDG QMVKLGLAHATLNIDDIQQAMALLSQSKD FR LVVHLLRTLQHGQPDELMLAMSL LTEYVQLFWTTAWPQNPLHKRRFAQQIL KRFDSSSFQSRADEAQRENVQGLLAHLA QVWHSREPLAKEVDALRSRYARPPERVIE AVASDEPLSSNTLAAAMAATPVSPSLAI DNTSDRAWRQTLLKMADLLSEQQPDAAI GFRLRHAVWGALTAPPMAQSDGRTPLAAV SADRTADYLARLANADLPLWHQVEQSLT LAPYWLDGHVLSAQIALQLGYDAVAQAIR D"

```

                                ELSVFLARIPALKTLFFTDMPFLSSESAAWLQQ
                                DANHQGRSRTIEQDEIWQCYQQQG
                                LEAALQMINRQPQQSEPRDRFYHQLLSAQLFEKA
                                GLTALAQQHYHSLLLVGQQLQLSE
                                WEPALIALLTEKQRQLKP"
gene      complement(292340..2930 /locus-tag="y0273"
35)
CDS      complement(292340..2930 /locus-tag="y0273"
35)
                                /note="residues 36 to 231 of 231
                                are 50.00 pct identical to
                                residues 47 to 244 of 247 from
                                GenPept :
                                >gb|AAG54522.1|AE005198-3
                                (AE005198) Z0253 gene product
                                [Escherichia coli O157:H7 EDL933]"
                                /codon-start=1
                                /transl-table=11
                                /product="hypothetical"
                                /protein-id="AAM83865.1"
                                /db-xref="GI:21956951"
                                /translation="MPAMNTWLLISSLLFSGGHT
                                DAFWTMGLPPPVAEKEEAGTLALV
                                MRCRSENSALVRLDCYDKALSPVNAVDEKRVNAG
                                PAWQRAMNQEKGRTDHSTAFLVTE
                                GEGSNPMVLITTPAIGMPPRPVLMMLSCIDNITR
                                LQIALVGPQKESSVTLIIDKAGII
                                DKTRLDAQWFLRENGYLLESSRGLAGIDEIKRLM
                                SAETLTIEGANGAFPRLTFTLSQL
                                TPALKPLRNACHW"
gene      complement(293023..2938 /locus-tag="y0274"
20)
CDS      complement(293023..2938 /locus-tag="y0274"
20)
                                /note="residues 194 to 260 of 265
                                are 29.57 pct identical to
                                residues 454 to 524 of 530 from
                                GenPept : >gb|AAF96031.1|
                                (AE004353) sigma-54 dependent
                                transcriptional regulator [Vibrio
                                cholerae]"
                                /codon-start=1
                                /transl-table=11
                                /product="hypothetical"
                                /protein-id="AAM83866.1"
                                /db-xref="GI:21956952"
                                /translation="MRQRLKSVLALLDNDSTEQL
                                IHRFLTINHHRQRFSA LMVSMFNA
                                SEGR LDCYHQPDGGMNVALKLDANIEDVNHPLVR
                                VLRNGFPEVWGS LYQGVRIEDDDF
                                RSFIQALPTRCGLYALPLFDVHGHACGVIAVFSE
                                NIERFADTRGIFSIYCHIFQHRLN
                                KLQEMDQLRSQFNQIRTVFKEQRQREKQLDELLV
                                SLSTSDTHALPGISQDYSKIDSLT
                                TAVETFECAVLTQRQRLYGNDKSRIAASLGLSLR
                                ALTYKLAKYRCQL"
gene      complement(293817..2964 /gene="clpB"
20)
                                /locus-tag="y0275"
CDS      complement(293817..2964 /gene="clpB"
20)
                                /locus-tag="y0275"

```

```

/function="putative enzyme;
degradation of proteins, peptides,
glyco"
/note="residues 153 to 857 of 867
are 40.22 pct identical to
residues 133 to 849 of 857 from E.
coli K12 : B2592; residues 1 to
866 of 867 are 67.25 pct identical
to residues 1 to 910 of 923 from
GenPept :
>gb|AAG54523.1|AE005198-4
(AE005198) putative protease
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="heat shock protein"
/protein-id="AAM83867.1"
/db-xref="GI:21956953"
/translation="MIQIDLPTLVNRLNPIARHS
LEAAAAHCVSQQEAEITVSQVLLQ
MISTPLCDVRLILSHAGVEEDELRESLDQRVSGY
QAITQAYPSFSPLLVEWLQDSWLL
ASTEMEHSQLRSGVMLLTLLLSPSRYLVP TANRL
LSPINRELLRQNFANWTADSAETP
RAEKGAEGNGAEINGDSLLARYASNMT EQARNG
ELDPVLCRDTEIDLMIDILCRRRK
NNPIVVGEGAGVGKSALIEGLALRIVDNQVPEKLR
NSELMTLDLGALQAGAAVKGEFEK
RFKGIMAEIAQSTTPIILFIDEAHTLIGAGNQQG
GLDISNLLKPALARGELKTIAATT
WSEYKKYFEKDAALSRRFQLVKVSEPSAQEATII
MRGLRTVYEQAHGVLIDDEALQAA
AVLSDRYISGRQLPDKAIDVLDTAAARVAINLTS
APRQVSALKNELYHQGMEIEMLER
EQRLSLSRPDERLSVLQQQRIEIEQQ LIALNTGW
EKQQHLVQQIIALRAVLLAQEESA
TDEQVVNLTALSDELERLQQHQTLVSPHVDKSQI
AAVIAEWTGVPLNRLSQSELAVVT
ELPSYLGQQIKGQETAIHCLHQHLLTARADLRPP
GRPMGAFLLVGPSGVGKTETVLQI
ADLLYGGRQYLTTINMSEFQEKHTVSRLIGSPPG
YVGYGEGGVLTEAIRQKPYSVLL
DEVEKAHPDVLNLFYQAFDKGELADGEGRIIDCK
NIVFFLTSLNGYQTIVDHADEPAL
LNERLYPELSAFFKPALLARMEVVPYLP LGMETL
QIIIHGKLNRLDTLLRQRF SADVV
IEPEVIDEILLRATRAENGARMLESIIDGALLPP
VSLLLLQKVAAGTAISHIRIAVEG
NVFTAQVEGAI "

```

gene complement (296431..2971 /locus-tag="y0276"
98)

CDS complement (296431..2971 /locus-tag="y0276"
98)

```

/function="putative membrane"
/note="residues 20 to 254 of 255
are 62.55 pct identical to
residues 18 to 252 of 253 from
GenPept :
>gb|AAG54524.1|AE005198-5
(AE005198) Z0255 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1

```

```

/translation="MKTDAVTDNTPFPAAEAVTS
HRQYQLPLRGESLNAMEIDTATPLL
GMVLRRLKDMENQALPDQLYQQVVTDIRAIEQYLQ
TKGYEPGAIISFRYVLCTFIDETA
LGHGWNTQNGWLQQSLLVHFHNETWGGEKVYVLL
ERLMGEPKRYQDLLEFIYLCFCLG
YRGYKVTSONGDDFERLFRRLHHQLQQLRGDAP
PTVLYQGGGRLNSRYHLSKRLTIK
HLLWGGVSLLVVIYLFYAIHLHTQSQDILQQLNN
LLS"
gene      complement(297198..2985 /locus-tag="y0277"
44)
CDS       complement(297198..2985 /locus-tag="y0277"
44)
/translation="MPTKNRVIWREGLFIKPQHF
QQQQRHNDYQLQRRRIALQGYRYG
FSSLILNQELLKLGRIGLTVASGNMADGTVFDIP
YQDYSPKPLDVLNCNDAASRDIYL
ALPMLNDAINVAGQQGQAPGTLRYREHSDDVRD
LHTEGGDVSQVLVAQLAPRLMQGS
EDLSAYSVLPLCRVKEKRPDGSILDEEFIPTCT
TLVSSTQLKGFMDVEGTLVERAQ
LLAKRIGSPGQQGIADVAEFMMLQVFNRTQPLFT
HLAQAILHPEAFYHQLVQTCGEL
RTFTDESRLAGTFPVYNHDNLDSFQPLFLAMRQ
ALSTVLTTPRAISIQLHMQAHGIRV
ATINDSDLLRSADFLAVRAQIPQEQLRRQFVQQ
TKITSLEKIRDLSVSVQLPGVPLVA
LSAAPRQLPYHSGYTYFMLDLQSPVWKEIQQSNA
IAFHVSGDFPDLDMQFWAIRSS"
gene      complement(298547..2990 /locus-tag="y0278"
92)
CDS       complement(298547..2990 /locus-tag="y0278"
92)
/translation="MPTKNRVIWREGLFIKPQHF
QQQQRHNDYQLQRRRIALQGYRYG
FSSLILNQELLKLGRIGLTVASGNMADGTVFDIP
YQDYSPKPLDVLNCNDAASRDIYL
ALPMLNDAINVAGQQGQAPGTLRYREHSDDVRD
LHTEGGDVSQVLVAQLAPRLMQGS
EDLSAYSVLPLCRVKEKRPDGSILDEEFIPTCT
TLVSSTQLKGFMDVEGTLVERAQ
LLAKRIGSPGQQGIADVAEFMMLQVFNRTQPLFT
HLAQAILHPEAFYHQLVQTCGEL
RTFTDESRLAGTFPVYNHDNLDSFQPLFLAMRQ
ALSTVLTTPRAISIQLHMQAHGIRV
ATINDSDLLRSADFLAVRAQIPQEQLRRQFVQQ
TKITSLEKIRDLSVSVQLPGVPLVA
LSAAPRQLPYHSGYTYFMLDLQSPVWKEIQQSNA
IAFHVSGDFPDLDMQFWAIRSS"

```

gene complement(299092..3004 /locus-tag="y0279"
08)
CDS complement(299092..3004 /locus-tag="y0279"
08)

/db-xref="GI:21956956"
/translation="MNNARGYLLTWALCVVFLLS
GCSGAWEATKKVGKVVMDPDIPVG
QATDQPSTVRLTLLSDPTNPNEKGEAVPTEIVV
VYLSENSKLLAADYDQLSSDALEK
TLGKNYIDHQEYTLTPDQFKALDPIKLEEKNSYL
GVIAHYADANRSEWKKI IKIGIG
HNYQVLVHVRSDVDLRKEEE"

/note="residues 2 to 438 of 438
are 45.47 pct identical to
residues 10 to 432 of 433 from
GenPept :
>gb|AAG54527.1|AE005198-8
(AE005198) Z0258 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83871.1"
/db-xref="GI:21956957"
/translation="MDKKQPTLSLRVNSDKLES
GKQASSLFHTQGGSVGSDGSHHWS
IQDQGGNISPSQFAIEWRDGSFCLRMLNGSLNIN
HSMLTPNSGFVRLQQGDEMTLGNL
VIKSHISRSAADMIDPLMVSPESLVSSYSNPMDA
MMEGEPLASPHHQQDSRLAATVSH
NFSHDPLRVLETESLTTQGHDAVISDADHSLQQD
RYRNPLFSSPLSDTPKDSAMDQAF
IDL PQISTFLNGKQAGGKPEGLNNQMEQHVAIT
PLMRGFDAQLP IRNSQEAHDFLEE
AGKTLKATIEGLLALQRSQHGLRDKHLRPIEDNP
LRLNMDYDTTLNLMFADQKSPVHL
SAPAAVAESLDNLRLLHHQANQQAITQALNTMLEA
FSPERLLTRFTHYLRSNRQE QDS
AWAWDMYKNYYNELASSRQQGFELFGEVYEQAY
DRALRQGMKDSE"

gene complement(300534..3016 /locus-tag="y0280"
31)
CDS complement(300534..3016 /locus-tag="y0280"
31)

/note="residues 44 to 363 of 365
are 57.89 pct identical to
residues 37 to 358 of 360 from
GenPept :
>gb|AAG54528.1|AE005198-9
(AE005198) Z0259 gene product
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83872.1"
/db-xref="GI:21956958"
/translation="MLRMAGTDRSTCTDVS VVED
VSGVENVNGVEARPEGQALDVSR Y
NFFQLVELLNQLAVAWQGAAPVATPANEAIRFKS
TASLAFPTRDVIALDTSARGQFEL
EVSFLGLHGSQSPLPGYYLDSLAWEDAQNENRLT
DFMNVFNHRLLTLLHQIWRKYRYY"

		ICFDNGGDDAFSQRMFSLVGLGSEVVRNKLQINH SKMLAYAGLLASPGRAPEVICSLV SHCFNLPDITLHSWQLRKVDIAPSQQNRLGTRVK VRGKKYDEKSVLGVNFSIGSRVAD RSGKFLLCINKLTREQFLSFLPNGANYASLVMFV AFIMRDQFAWDLRLGLAEQQVGGM VLGTEQNSLLGWTASILGDPEQKPSVTIGVME"
gene	complement(301586..302458)	/locus-tag="y0281"
CDS	complement(301586..302458)	/locus-tag="y0281"
		/note="residues 46 to 290 of 290 are 55.51 pct identical to residues 345 to 589 of 589 from GenPept : >gb AAF96024.1 (AE004353) hypothetical protein [Vibrio cholerae]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83873.1" /db-xref="GI:21956959" /translation="MRFPAEWPFLKGNVEPPLGG LKKGVSLNRTSRSWIKRSKIWGSV HRGHGREYTSFESFHHQIEHSQEKTALYYRLRVK NSLFRKGFHYISFVRSDESKLVL AEENVSVSLTCTNRELPLSLRVGDINQLSTDSPS FATFRNITRPSVPLYPVLDGGLHW SLLSNMSLNYMSLLDKDALKQILHTYDFPSLHNR QSARASQKKLDAIQRIETQPIDRL FRGLPVRGLQTTLWLEQGAFSSEGELYLFSTVLA RFFSLYASVNAFHLLKVINLDNQE CYEWPVQTGQHALLM"
gene	302218..302895	/locus-tag="y0282"
CDS	302218..302895	/locus-tag="y0282"
		/function="IS and transposon related functions" /note="IS1661 transposase; residues 56 to 224 of 226 are 39.64 pct identical to residues 1 to 167 of 173 from GenPept : >emb CAA63546.1 (X92970) orfA [Escherichia coli]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83874.1" /db-xref="GI:21956960" /translation="MNFSHVGGNKVRSFLASVRS DGGSSQTRCTPGHDPGALNPRSWI FLSMIWRFGSMKHPFSTRLAHVQHYLSGKATLRE TARQFSVGKSPLTRWIRAFRRQGE AGLEHHLSTRYTPEFRLCVVRYMMANRCSAADAS AHFNIPNETIIQNWMKRYREGGKE ALNPSKTGPTMPKDKYEHDSKPFSEMTHAELEKE LEYLRAENAYLKKRKALREEKALR EQQKKPE"
repeat-region	302324..303509	/note="insertion element; partial" /insertion-seq="IS1661"
gene	302949..303569	/locus-tag="y0283"
CDS	302949..303569	/locus-tag="y0283"
		/function="IS and transposon related functions"

		/note="IS1661 transposase; residues 3 to 187 of 206 are 45.74 pct identical to residues 24 to 207 of 283 from GenPept : >gb AAB18535.2 (U00039) orfB in IS150 [Escherichia coli]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83875.1" /db-xref="GI:21956961" /translation="MARSTYYYHASKPDGVIDDY ADAVKAIGALSRRHAQRYGYRRMT VALRKEGFTLNHKTVRKLMNQHGLLSLIRKKYR SYRADGGRASDNLLARNFTSEISG LKWCTDVTEFRVGAQKLYLSVIQDLFNNEIISWH MSERAALILTCKTLEKALKVKGRK EGLMLHSDQGWHYRTPMWRSMLEAGICNERCNS DPHPTPEIRSRG"
repeat-region	303510..305463	/note="insertion element" /insertion-seq="IS100"
gene	303596..304618	/locus-tag="y0284"
CDS	303596..304618	/locus-tag="y0284" /function="IS and transposon related functions" /note="IS100; orfA; residues 1 to 340 of 340 are 100.00 pct identical to residues 1 to 340 of 340 from GenPept : >gb AAC13168.1 (AF053947) putative transposase [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83876.1" /db-xref="GI:21956962" /translation="MVTFETVMEIKILHKQGMSS RAIARELGISRNTVKRYLQAKSEP PKYTPRPAVASLLDEYRDYIRQRIADAHYPKIPA TVIAREIRDQGYRGGMTILRAFIR SLSVPQEQEPAVRFEFETEPGRQMVDWGTMNRGRS PLHVFVAVLGYSRMLYIEFTDNMR YDTLETCHRNAFRFFGGVPREVLYDNMKTIVVLQR DAYQTGQHRFHPSLWQFGKEMGFS PRLCRPFRAQTKGKVERMVQYTRNSFYIPLMTRL RPMGITVDVETANRHGLRWLHDVA NQRKHETIQARPCDRWLEEQQSMLALPPEKKEYD VHLDENLVNFDKHPLHHPLSIYDS FCRGVA"
gene	304615..305397	/locus-tag="y0285"
CDS	304615..305397	/locus-tag="y0285" /function="IS and transposon related functions" /note="IS100; orfB; residues 1 to 260 of 260 are 100.00 pct identical to residues 1 to 260 of 260 from GenPept : >gb AAC69770.1 (AF074612) putative transposase [Yersinia pestis]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83877.1"

		/db-xref="GI:21956963" /translation="MMELQHQRMLMALAGQLQLE SLISAAPALSQQAVDQEWSYMDFL EHLLHEEKLARHQKQAMYTRMAAFPAVKTFEY DFTFATGAPQKQLQSLRSLSFIER NENIVLLGPSGVGKTHLAIAMGYEAVRAGIKVRF TTAADLLLQLSTAQRQGRYKTTLQ RGVMAPRLLIIDEIGYLPFSQEEAKLFFQVIKR YEKSAMILTSNLPFGQWDQTFAGD AALTSAMLDRIHHSHVQIKGESYRLRQKRKAG VIAEANPE"
repeat-region	complement(305463..305663)	/note="insertion element; partial"
gene	complement(305910..308024)	/insertion-seq="IS1541a" /locus-tag="y0286"
CDS	complement(305910..308024)	/locus-tag="y0286" /function="putative membrane; transport of small molecules; cations" /note="similar to colicin V secretion ATP-binding protein CvaB; residues 1 to 698 of 704 are 57.16 pct identical to residues 1 to 698 of 698 from GenPept : >gb AAL08400.1 (AF063590) MceG [Klebsiella pneumoniae]" /codon-start=1 /transl-table=11 /product="putative secretion ATPase" /protein-id="AAM83878.1" /db-xref="GI:21956965" /translation="MNDTHFNEIKNRLNFSFRK VPQVLQTEAAECGLACLVMTCRYH GMDIDLFNLRQRFGISSHGATLALLINISAQLKF KTRALSDDLDELRLQKTPCILHWD MSHFVVLVAVKGTRFIIHDPAFGRRTVSLSEMSQ HFTGVALELWPNSEFTRQKSRTLL SLLSLMRNISGLPGFLTKIFCLSLMVEAINLLLLP VGTQLVMDHVIIAEDYDLLALICI GLLFFILFRTFLSMLRSWTSVMGSLVDVQWKAG LFDHLLKLPLAYFEKRKLGDIIQSR FGSLDIIRSTLTNNVNGIIDGLMSIGVFIMMFL YGGWLWVVLGFTAMYMILRLATY NQYRQASEEQIVKNAKASSHFMETLYGISTLKAL GLAATRSQFWLNLNIDTTNANIRL TKLDMFFGGVNTLIGTIDQVILWLGLASMVIDGQ MTLGMFVAFNAYRGQFSDRATNLI NMVLQLRMLALHSERIADIVFTETEKEQTPRQLL SPNQPAVFEARNIAFYDNLSKPI FSDLNIHVEAGESVAITGPSGIGKTTLMKVIAGL LTPSQGHILIDGLDITTVGLNNYR DCIACVLQDDKLFAGSIADNIASFVNVKDEQRIL SCANHCNIHKEIMHMPMGYETLIS ELGGSLSGGQKQRLLIARALYRQPSLLFLDEATS HLDLANEAHINNAIASLKITRIFI AHRPSTIASAQRIINLEKQNVS"
gene	complement(308017..309333)	/locus-tag="y0287"
CDS	complement(308017..309333)	/locus-tag="y0287"

33)

		<pre> /function="putative membrane; transport of small molecules; cations" /note="similar to colicin V secretion protein CvaA; residues 14 to 438 of 438 are 47.05 pct identical to residues 1 to 424 of 424 from GenPept : >emb CAC21493.1 (AJ278866) MchE protein [Escherichia coli]" /codon-start=1 /transl-table=11 /product="putative secretion permease" /protein-id="AAM83879.1" /db-xref="GI:21956966" /translation="MMGITERGMSSNQIFRRDAV EYIRTKWLGKALLTSGYSTTFIAA LCAIFLVLLITLIIYGTYTTRRINVNGEVISQPHP INIFSPQQGFITKKWVEVGDIVRK GQHLYQIDVSRTTFSGNVSLNSLEAINNQLSQID SIINNTQKNKELTLLNLRQQLAQY QKAHKKSQELVDNAGKGMDDMRRTMASYGTYQRQ GLITKDQLTNQRSIFYQQNAFQS LNTQLIQESLQIAKLESEISTRASDFDNDISQYL FQKGDLLKRLAEVDASGMLLINSP SDGKIENMSVTQGMVNVNDSLVLTPSDNPYYC LVLWVPNNSVPYINTGDKVNIRYD AFPFEKFGQFPGRIISISNVPVSQQEIASYNIAP RLPNGGLIEPYKVIIVALDDIHR YQSKPLMLSNGLKANVTFLFLEKRPLYQWMLSPFY DIKKSVTGPVNE" </pre>
gene	309522..309761	/locus-tag="y0288"
CDS	309522..309761	/locus-tag="y0288"
		<pre> /note="residues 12 to 72 of 79 are 31.14 pct identical to residues 383 to 440 of 657 from GenPept : >gb AAB18717.1 (U38906) ORF42 [Bacteriophage rlt]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83880.1" /db-xref="GI:21956967" /translation="MKELTQTEVMEVSGAGIVSD AGKVLGSGFGALIDAGASIFGIKP NASATIGKIGESIGSAFDAGISGVKQFFGLSAPQ Q" </pre>
gene	309936..310085	/locus-tag="y0289"
CDS	309936..310085	/locus-tag="y0289"
		<pre> /note="residues 7 to 48 of 49 are 26.19 pct identical to residues 262 to 303 of 355 from GenPept : >gb AAF98228.1 (U64843) hypothetical protein K06C4.8 [Caenorhabditis elegans]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83881.1" /db-xref="GI:21956968" </pre>

		/translation="MKIAYRTIRFINLWIYAVFY SEFFGFELSHYLSTADMIFFGDYE FILYH"
gene	complement(310351..310512)	/locus-tag="y0290"
CDS	complement(310351..310512)	/locus-tag="y0290"
		/note="residues 4 to 40 of 53 are 37.83 pct identical to residues 159 to 195 of 195 from GenPept : >emb CAC09571.1 (AJ298983) S-receptor kinase (SRK) [Fagus sylvatica]"
		/codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83882.1" /db-xref="GI:21956969" /translation="MACSDFACSEIAHADTDSVM ATIKATPAVVVLRRKQQPLCIKKP HQDVNELSQ"
gene	310544..310975	/locus-tag="y0291"
CDS	310544..310975	/locus-tag="y0291"
		/note="residues 10 to 30 of 143 are 66.66 pct identical to residues 1017 to 1037 of 1263 from GenPept : >gb AAG31016.1 (AY007367) tospovirus resistance protein D [Lycopersicon esculentum]"
		/codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83883.1" /db-xref="GI:21956970" /translation="MAHLNARFDDKEGLFEGASQ SGTLLILRNISARACQVNAMPVIS FEGAVGQQLAVFRKQVPRGMRQEPVLSPTVAAGA EVAVQLRWVASDAFDGNNCVTPEK VVVTLLGGTLRLPFGQMCAASGDTEFFSQAPVG PATNEVQ"
gene	complement(311092..311577)	/gene="menG"
		/locus-tag="y0292"
CDS	complement(311092..311577)	/gene="menG"
		/locus-tag="y0292"
		/function="putative enzyme; biosynthesis of cofactors, carriers: Menaquinone, ubiquinone"
		/note="menaquinone biosynthesis; residues 1 to 161 of 161 are 87.57 pct identical to residues 1 to 161 of 161 from E. coli K12 : B3929"
		/codon-start=1 /transl-table=11 /product="2-heptaprenyl-1,4-naphth oquinone methyltransferase"
		/protein-id="AAM83884.1" /db-xref="GI:21956971" /translation="MKYDTSDLCDIYHEEVNVVE PLFSNFGGRTSFGGKITTVKCFED NGLLFDLLEENGLGRVLVVDGGGSVRRALINAEI

		AELALKNEWEGIVVYGAVRQVDDL AELDIGIQAMAAIPVGAADGEGVGESDIRVNFGGV TFFSGDHLIYADNTGIILSEDPLDI E"
gene	complement (311719..312648)	/gene="menA"
		/locus-tag="y0293"
CDS	complement (311719..312648)	/gene="menA"
		/locus-tag="y0293"
		/function="enzyme; biosynthesis of cofactors, carriers: Menaquinone, ubiquinone"
		/note="1,4-dihydroxy-2-naphthoate --> dimethylmenaquinone; residues 12 to 309 of 309 are 68.12 pct identical to residues 7 to 304 of 308 from E. coli K12 : B3930; residues 12 to 309 of 309 are 69.12 pct identical to residues 8 to 305 of 309 from GenPept : >gb AAL22930.1 (AE008891) 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Salmonella typhimurium LT2]"
		/codon-start=1
		/transl-table=11
		/product="1,4-dihydroxy-2-naphthoate octaprenyltransferase"
		/protein-id="AAM83885.1"
		/db-xref="GI:21956972"
		/translation="MKRKMSLSINTSQTQAWLES LRPRTLPLAFASIVTGSALAVWLD SFKPAVALLALLTAGLLQILSNLANDYGDVKGSDTEERIGPLRGMQKGIISHQQMKV ALIITVILTIISGIALIAVACEKPSDILGFLLLGLMAIVAAITYTVGRKPYGYMGLGD ISVLVFFGWLSVAGTYYLQAGHFDSIVMLPATAC GLLATAVLNINNLRDIENDKANGK NTLAVRLGPVVARYYHALLIGAAIFCLALFSILHLHSHWGWIFLLAIPLLGKHALFVL RDPTAAGMRPMLEQMVKAALLTNILFAVGLVFS"
gene	complement (312872..314203)	/gene="hslU"
		/locus-tag="y0294"
CDS	complement (312872..314203)	/gene="hslU"
		/locus-tag="y0294"
		/function="factor; adaptations, atypical conditions"
		/note="homologous to chaperones; residues 1 to 443 of 443 are 90.29 pct identical to residues 1 to 443 of 443 from E. coli K12 : B3931"
		/codon-start=1
		/transl-table=11
		/product="heat shock protein, ATPase subunit"
		/protein-id="AAM83886.1"
		/db-xref="GI:21956973"
		/translation="MSEMPREIVSELDSHIIGQDKAKRAVAIALRNRWRMQLNEEL RHEVTPKNILMIGPTGVGKTEIARRLAKLANAPF"

```

IKVEATKFTTEVG YVGKEVDSIIRD
LTDAAVKMVRHQSI EKMR YRAEELAEERILDVLI
PPAKNNWGV PDESQEPSATRQTFR
KKLREGQLDDKEIEIDLAAAPMGVEIMAPPGMEE
MTNQLQSMFQNIAGQKQKPRKIKI
KEALKLLIEEEAAKLVNPEELKQQAIDAVEQHGI
VFIDEIDKICKRGQTSGPDVSREG
VQRDLLPLVEGCTVSTKHGMVKTDHILFIASGAF
QVSSPSDLIPELQGR LPIRVELQA
LTDDFERILTEPSASLTEQYKALMATEGVTIEF
TREGIRKIAEAAWQVNERTENIGA
RRLHTVLERLMEDISYDASESSGQSITIDAEYVG
KHLDELVADEDLSRFIL"

gene      complement(314274..3147 /gene="hslV"
98)

CDS      /locus-tag="y0295"
complement(314274..3147 /gene="hslV"
98)

/locus-tag="y0295"
/function="enzyme; degradation of
proteins, peptides, glyco"
/note="residues 1 to 174 of 174
are 90.80 pct identical to
residues 1 to 174 of 176 from E.
coli K12 : B3932; residues 1 to
174 of 174 are 100.00 pct
identical to residues 1 to 174 of
174 from GenPept :
>emb|CAC88971.1| (AJ414141) heat
shock protein [Yersinia pestis]"
/codon-start=1
/transl-table=11
/product="heat shock protein,
proteasome-related peptidase
subunit"
/protein-id="AAM83887.1"
/db-xref="GI:21956974"
/translation="MTTIVSVRRDGHVVIGGDGQ
VTLGNTVMKGNNAKKVRRRLYNNKVI
AGFAGGTADAFTL FELFERKLEMHQGHLTKAAVE
LAKDWRTDRMLRKLEALLAVADET
ASLIITGNGDVVQPEDDLIAIGSGGPYAQSAARA
LLENTELGARDIVEKSLSIAGDIC
IYTNRFTQIEELTY"

gene      complement(314898..3157 /gene="ftsN"
43)

CDS      /locus-tag="y0296"
complement(314898..3157 /gene="ftsN"
43)

/locus-tag="y0296"
/function="phenotype; cell
division"
/note="residues 1 to 281 of 281
are 49.68 pct identical to
residues 1 to 319 of 319 from E.
coli K12 : B3933; residues 1 to
281 of 281 are 51.38 pct identical
to residues 1 to 324 of 324 from
GenPept : >gb|AAL22933.1|
(AE008891) essential cell division
protein [Salmonella typhimurium
LT2]"

```

		/codon-start=1 /transl-table=11 /product="essential cell division protein" /protein-id="AAM83888.1" /db-xref="GI:21956975" /translation="MAQRDYVSRGRSGARRKSTS RKKRSAPIVSKTVMALAVALLVVF VGGLYFITHNKPGEPLLPNNDPRTGNGLPKPKE ERWRYIKELENRQIGVPMPTEPSA GGEVNAKTELTNEQRQLLEQMADMRRQPTQLSE VPYNQGMQQVPRSAVTIKPPATSV QPQPVTTPRQTTIPVQPQAPAPVRTPPAAPVTQA VTPPKVEKEKEKTQRWMVQCGSFK AVDQAESIRAQLAFAGIESRITSGGGWNRVVLGP YNSKAAADKALQRLQGAGQSGCIP LSVGG"
gene	complement(315809..316837)	/gene="cytR"
CDS	complement(315809..316837)	/locus-tag="y0297" /gene="cytR" /locus-tag="y0297" /function="regulator; global regulatory functions" /note="residues 1 to 339 of 342 are 71.38 pct identical to residues 1 to 339 of 341 from E. coli K12 : B3934" /codon-start=1 /transl-table=11 /product="regulator for deo operon, udp, cdd, tsx, nupC, and nupG" /protein-id="AAM83889.1" /db-xref="GI:21956976" /translation="MENKKEFTMTTMKDVAEMAG VSTATVSRALMNPEKVSTVTRQKV EQAVLAVGYSPHALSRNIKRNESRTILVIVPDIS DPFFADVIGGIEHAAAQQGYLILI GDCAQQTQQERTFVNLIITKQIDGMLLLGSNLFP DASKEEQRNLPMMVMANFAPELE LPTVHIDNLTAAYEAVNYLHELGHKRIACIAGPE SLPLSHYRLQGYIQALRRNGITVD NDYIIRGDFS YEAGAQSF AALMELPHPPTAIFSH NDVMAVGAIWQAKQLGLRIPQDVS LVGFDDLKLSQFCDPPLTTVAQPRYQIGQQAMLL LLEQLQGHSVQSGSRLLDTELIIR ESTAAPKH"
gene	complement(317190..319388)	/gene="priA"
CDS	complement(317190..319388)	/locus-tag="y0298" /gene="priA" /locus-tag="y0298" /function="factor; DNA - replication, repair, restriction/modification" /note="factor Y; putative helicase; residues 1 to 731 of 732 are 73.08 pct identical to residues 1 to 731 of 732 from E. coli K12 : B3935; residues 1 to 731 of 732 are 72.67 pct identical

		to residues 1 to 731 of 732 from GenPept : >gb AAL22935.1 (AE008891) primosomal protein N' (= factor Y) directs replication fork assembly at D-loops [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="primosomal protein N'" /protein-id="AAM83890.1" /db-xref="GI:21956978" /translation="MSVVQVALPVPLARTFDYRL DSAMACPVVGARVSVFPGKRKAIG IVVGLSDTSTFPLEQLKTIDAILDNHSLFPPSLW RILCWATEYYHYPIGEVLFHALPI LLRQGRPAQSAPLWQWFVTEQGRATPPESLKRAP KQQQALAALLQKPVYRHQVNEMAL TESALQALRSKGLIDLRAQEATTTDWRHSFSVLG ERLRLNTEQATAVGAIKSEDNQFA AWLLAGVTGSGKTEVYLSVLENILAQGRQALILV PEIGLTPQTIARFRERFNAPVEVL HSGLNDSERLSVWLRARSGEAAIVIGTRSAFTF FSR LGV I I I D E E H D S S Y K Q Q E G W R YHARDLAVFRAREEGIPVIMGTATPALET L H N V Q MGKYRQLTLTKRAGSAKPAAQHLL DLKGLPLKVGLSQPLLKQMKTHLQAGNQVILFLN RRGYAPALLCHECGWIAECQRCDH YYTLHQNHRQLRCHHCDSQRPVPQQCPKCGSTHL VSVGVGTEQLENELAPLPETPIT RIDRDTTSRKGSLEQYLADVHQGGARILIGTQML AKGHHFPDVT L V A L L D V D G A L F S A DFRSAERFAQLYTQVSGRAGRAGKQGEVILQTHH PEHPLLQILLQQGYDAFAKQALEE RKS V F L P P Y T S H I I V R S E D H D N Q Q S A L F L Q Q L R N L L E A S P L K D E A L W I M G P V P A L Q A K R G G R F R W Q L L L Q H P S R Q L L Q R L I K T S Q P L I S T L P Q A R K V K W T I D V D P I D S "
gene	319574..319846	/gene="rpmE"
		/locus-tag="y0299"
CDS	319574..319846	/gene="rpmE"
		/locus-tag="y0299"
		/function="structural component; ribosomal proteins - synthesis, modification"
		/note="residues 20 to 89 of 90 are 81.42 pct identical to residues 1 to 70 of 70 from E. coli K12 : B3936"
		/codon-start=1
		/transl-table=11
		/product="50S ribosomal subunit protein L31"
		/protein-id="AAM83891.1"
		/db-xref="GI:21956979"
		/translation="MWCLAEQGWIA TRPNIEVSM KQGIHPKYEQVTASCSCGNVIKIN STVGHDLNLDVCGECHPFYTGKQRDVASGGRVDR FNKRFSVPGAKK"
gene	complement(320371..320838)	/locus-tag="y0300"
CDS	complement(320371..320838)	/locus-tag="y0300"

		<p>/note="residues 13 to 140 of 155 are 65.62 pct identical to residues 10 to 137 of 146 from E. coli K12 : B3562; residues 5 to 150 of 155 are 57.53 pct identical to residues 1 to 146 of 166 from GenPept : >emb CAD13669.1 (AL646057) hypothetical transmembrane protein [Ralstonia solanacearum]"</p> <p>/codon-start=1</p> <p>/transl-table=11</p> <p>/product="hypothetical protein"</p> <p>/protein-id="AAM83892.1"</p> <p>/db-xref="GI:21956980"</p> <p>/translation="MDLNMNPNYAKPSAAFTAASWSALLGGFVIFLIGLWNADMQLNE RGYFFAVLILGLFSAVSLQKTVRDKLEGLAITSIYYGLCWVAFIVAVLLLCIGLWNAT LALSEKGFYGVTFMTLFGAIAVQKNTRDSAMSSDTESASLFFKKVRDQLKAED"</p>
gene	complement(321175..321492)	/gene="metJ"
CDS	complement(321175..321492)	<p>/locus-tag="y0301"</p> <p>/gene="metJ"</p> <p>/locus-tag="y0301"</p> <p>/function="regulator; amino acid biosynthesis: Methionine"</p> <p>/note="residues 1 to 105 of 105 are 89.52 pct identical to residues 1 to 105 of 105 from E. coli K12 : B3938; residues 1 to 105 of 105 are 91.42 pct identical to residues 1 to 105 of 105 from GenPept : >gb AAL22939.1 (AE008891) transcriptional repressor of all met genes but metF (MetJ family) [Salmonella typhimurium LT2]"</p> <p>/codon-start=1</p> <p>/transl-table=11</p> <p>/product="repressor of all met genes but metF"</p> <p>/protein-id="AAM83893.1"</p> <p>/db-xref="GI:21956981"</p> <p>/translation="MAEWNGEYVSPYAEHGKSKQVKKITVSIPLKVLKILTDERTRRQVNNLRHATNSELLCEAFLHAFTGQQLPNDEDLRKERSDEIPEAAKILMRELGVDPDT WEY"</p>
gene	321789..323029	<p>/locus-tag="y0302"</p> <p>/note="metB; disrupted by frameshift"</p>
gene	323032..325467	<p>/pseudo</p> <p>/gene="metL"</p>
CDS	323032..325467	<p>/locus-tag="y0303"</p> <p>/gene="metL"</p> <p>/locus-tag="y0303"</p> <p>/function="enzyme; amino acid biosynthesis: Methionine"</p> <p>/note="residues 8 to 811 of 811 are 83.95 pct identical to</p>

residues 7 to 810 of 810 from E.
coli K12 : B3940; residues 8 to
811 of 811 are 83.95 pct identical
to residues 7 to 810 of 810 from
GenPept :

```
>gb|AAG59141.1|AE005625-4
(AE005625) aspartokinase II and
homoserine dehydrogenase II
[Escherichia coli O157:H7 EDL933]"
/codon-start=1
/transl-table=11
/product="aspartokinase II and
homoserine dehydrogenase II"
/protein-id="AAM83894.1"
/db-xref="GI:21956982"
/translation="MNATAVAAAATGRQLHKFGG
SSLADVKCYLRVANIMANYSHPGD
LMVVSAAAGSTTNQLISWLKLSQNDRLSAHQVQQS
LRRYQHDLINGLLPPEMAEPLISE
FIHDLERLAGLLDNKIDDVIIYAEVVGHGEIWSAR
LMSALLNKLDMDAVWLDARRFLRA
ERAAQPQIDESRSYPLLQQLMAQHPHQRLVVTGF
ISRNEAGETVLLGRNGSDYSATQV
GALAGAERTVIWSDVAGVYSADPRKVKDACLLPL
LRLDEASELARLAAPVLHTRTLQP
VSGSDIDLQLRCSYQPEQGSTRIERVLASGLGAK
IVTSHDDVCLIELQIASHHDFSLA
QKEIDLLLKRAQIKPLATGIHPDRNLLQLCYTSE
VVNSALRVLEDAALPGKLSLREGL
ALVALVGAGVSKNPLHSHRFYQQLKDQPVFEVWQ
AEDGISMVAVLRLGPTHEHLIQGLH
QSLFRAEKRIGLMLFGKGNIGARWLELFAREQKS
LSARSGFEFVLAVVDSRRSLLSY
DGLDASRTLAFYNDEAKEQDEESLFLWMRAHPFD
DLVVLDVTASPSLAEQYLDFASYG
FHVISANKLAGASSSNNYRQIRDAFAKTGRHWLY
NATVGAGLPVNHTVRDLRDSGDSI
LAISGIFSGTLSWLFLQFDGSPFTTELVDQAWQQ
GLTEPDPRVDLSGQDVMRKLVLILA
REAGYDIEPNQVRVESLVPAGAESGSVDQFFENG
EALNQQMIQRLEAAKEMGLVLRVY
ARFDANGKARVGVEAVRTDHPASLLPCDNVFAI
ESRWYRDNPLVIRGPGAGRDVTAG
AIQSDLNRLSQLL"
```

gene 325700..326584

CDS 325700..326584

```
/gene="metF"
/locus-tag="y0304"
/gene="metF"
/locus-tag="y0304"
/function="enzyme; central
intermediary metabolism: Pool,
multipurpose conversions"
/note="residues 1 to 294 of 294
are 86.39 pct identical to
residues 1 to 294 of 296 from E.
coli K12 : B3941; residues 1 to
294 of 294 are 91.83 pct identical
to residues 1 to 294 of 298 from
GenPept : >gb|AAC72242.1| (U74302)
5,10-methylenetetrahydrofolate
reductase [Pectobacterium
carotovorum]"
/codon-start=1
```


		/transl-table=11 /product="5,10-methylenetetrahydrofolate reductase" /protein-id="AAM83895.1" /db-xref="GI:21956983" /translation="MSFFHANQREALNQSLSELQ GQINVSFEFFPPRTSEMEDTLWSS IDRLSTLKPKFVSVTYGANSGERDRTHSIIKGIK ERTGLEAAPHLTCIDASPTQLRDI AIDYWNSGIRHIVALRGDLPPNSGKPEMYACDLV GLLKDVGDFDISVAAYPEIHPEAK SAQADLINLKRKIDAGANRAITQFFFDVESYLRF RDRCVATGIDVEIVPGILPVSNFK QLQRFATMTNVRVPNWMTSIFDGLDNDPETRKMV GASVAMDMVKILSREGVKDFHFYT LNRAELSYAICHTLGVPR"
repeat-region	complement(326721..328172)	/note="insertion element"
gene	complement(326762..327361)	/insertion-seq="IS1661" /locus-tag="y0305"
CDS	complement(326762..327361)	/locus-tag="y0305" /function="IS and transposon related functions" /note="IS1661 OrfB transposase; residues 1 to 198 of 199 are 54.54 pct identical to residues 41 to 238 of 240 from GenPept : >emb CAA63547.1 (X92970) orfB [Escherichia coli]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83896.1" /db-xref="GI:21956984" /translation="MNQHGLLSLIRRKYSYRA DGGRASDNLLARNFTSEISGLKWC TDVTEFRVGAQKLYLSVIQDLFNNEIISWHMSER AALILTCKTLEKALKVKGRKEGLM LHSDQGWHYRTPMWRSMLEAGIRQSMSRKGNCL DNAVMENFFSHLKAEMYHRKKYDS ATVLKRDIVEYIHYNTERISLKTGGMSPAERYT QVEKQ"
gene	complement(327602..328243)	/locus-tag="y0306"
CDS	complement(327602..328243)	/locus-tag="y0306" /function="IS and transposon related functions" /note="IS1661 DNA-binding protein; residues 43 to 211 of 213 are 39.64 pct identical to residues 1 to 167 of 173 from GenPept : >emb CAA63546.1 (X92970) orfA [Escherichia coli]" /codon-start=1 /transl-table=11 /product="putative transposase" /protein-id="AAM83897.1" /db-xref="GI:21956985" /translation="MNRGNPRSGOAIVRKRGVPR"

		GPRFALNPRSWIFLSMIWRFGSMK HPFSTRLAQVHYLSGKATLRETARQFSVGKSPL TRWIRAFRRQGEAGLEHHLSTRYT PEFRLCVVRYMMANRCSAADASAHFNIPNETIIQ NWMKRYREGGKEALNPSKTGPTMP KDKYEHDSKPFSEMTAELEKELEYLRAENAYLK KRKALREEKALREQQKKPE"
gene	328492..328707	/locus-tag="y0307"
CDS	328492..328707	/locus-tag="y0307" /note="residues 3 to 66 of 71 are 32.30 pct identical to residues 328 to 389 of 550 from GenPept : >gb AAB88471.1 (AF242881) agaG [Agrobacterium tumefaciens]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83898.1" /db-xref="GI:21956987" /translation="MTLSAIRNIADKERGASERA WTPAKSALGQGCPSRWLVSPPKADG GLPAGQYFAQAAGAGGPASPPARLRRL"
gene	complement (328859..3315 55)	/gene="ppc" /locus-tag="y0308"
CDS	complement (328859..3315 55)	/gene="ppc" /locus-tag="y0308" /function="enzyme; energy metabolism, carbon: Fermentation" /note="residues 21 to 898 of 898 are 82.10 pct identical to residues 1 to 883 of 883 from E. coli K12 : B3956; residues 21 to 898 of 898 are 82.10 pct identical to residues 1 to 883 of 883 from GenPept : >dbj BAB38308.1 (AP002567) phosphoenolpyruvate carboxylase [Escherichia coli O157:H7]" /codon-start=1 /transl-table=11 /product="phosphoenolpyruvate carboxylase" /protein-id="AAM83899.1" /db-xref="GI:21956988" /translation="MNIASNPAASNTKDKWVRGH MNEQYSAMRSNVSMGLTLLGDTIK EALGEHILDRVETIRKLSKSSRAGNEASRQELLT TLQNLNDELPLVARAFSQFLNLT NTAEQYHSISPHEAASNPEALAQFLTRLKDKKL SDQDMRSVDDLSIELVLTAPTE ITRRTLIIHKLVEVNTCLSQLDHNDLADYERNKIM RRLRQLVAQSWHTDEIRKLSPV DEAKWGFVAVVNSLWEGVPAFLREFNEQLENSLD YRLPVEAVPIRFTSWMGDRDGNP NVTAEITRHVLLLSRWKATDLFLRDIQVLVSELS MSECTPELRELAGEEVLEPYRQL MKNVRTQLTNTQAYLEARLKGERVLPDHLVSN DQLWEPLYACYQSLKACGMEIIAN GQLLDTLRRVRCFVPLVRIDVRQESTRHTDAIA ELTRYLGLGDYESWSESDKQAFV"

		RELNSKRPLVPLKWEPSAETQEVLETCRVIAEAP QGSIAAYVISMAKVPSDVLAVHLL LKEAGCPFTLPVAPLFETLDDLNNADDVMTQLLG IDWYRGLIQGQMVMIGYSDSAKD AGVMAASWAQYRAQDALIKTCEKAGITLTLFHGR GGSIGRGGAPAHAALLSQPPGSLK GGLRVTEQGEMIRFKFGLPEVTISSLALYAGAIL EANLLPPEPKKEWIEVMDLLSDA SCDMYRSYVRENPEFVRYFRAATPELELGKLPLG SRPAKRRPDGGVESLRAIPWIFAW TQNRLMLPAWLGAAGLQRAIDAGKQDVLATMCR DWPFFSTRIGMLEMVFAKADLWLA EYYDQRLVDKSLWPLGQQLRDQLAADIKVVLAIA NDDHLMADLPWIAESIALRNVYTD PLNVLQAELLHRSRQQEHPDACVEQALMVTIAGV AAGMRNTG"
gene	complement (331869..333038)	/gene="argE"
CDS	complement (331869..333038)	/locus-tag="y0309" /gene="argE" /locus-tag="y0309" /function="enzyme; amino acid biosynthesis: Arginine" /note="residues 1 to 386 of 389 are 77.72 pct identical to residues 1 to 381 of 383 from E. coli K12 : B3957" /codon-start=1 /transl-table=11 /product="acetylornithine deacetylase" /protein-id="AAM83900.1" /db-xref="GI:21956989" /translation="MKMKLPPIELYRALIATPS ISAADSALDQSNEALINLLAGWFA DLGFRVEIQVPDTRHKFNLLASIGENENGEGHG GLLLAGHTDTPYDEGRWTRDPFT LTEHDKLYGLGTADMKGFFAFILDAVRDIDASK LTKPLYILATADEETTMAGARYFA ANTQLRPDFAIIGEPTSLQPVRAHKGHISNAIRI TGQSGHSSDPARGVNAIDLMHESI TQLMALRTTLQERYHNPAFTIPYPTMNFHGINGG DAANRICACCELHMDIRPLPGLTL SDLNELMTEALEPVSQRWPGRLSIDELHPPPIPGY ECPTDHHMVGVIKLLGERTAVVN YCTEAPFIQQVCPTLVLGPGSINQAHQPDEFIDM AFIEPTRELIGQLVDHFCQQK"
gene	333283..334287	/gene="argC"
CDS	333283..334287	/locus-tag="y0310" /gene="argC" /locus-tag="y0310" /function="enzyme; amino acid biosynthesis: Arginine" /note="residues 1 to 334 of 334 are 78.14 pct identical to residues 1 to 334 of 334 from E. coli K12 : B3958" /codon-start=1 /transl-table=11 /product="N-acetyl-gamma-glutamylphosphate reductase"

		<pre> /protein-id="AAM83901.1" /db-xref="GI:21956990" /translation="MLNTLIVGASGYAGAELTAY LNRHPHMNITGLAVSAQSADAGKL LSDLHPQLKGILDPLQPLVDVAQAAKGIDVVFL ATAHEVSHDLAPQFLAAGCVVFDL SGAFRVRDAAFYSQYYGFEHQHPDWLDKAVYGLA EWQSEDIKQAQLIAVPGCYPTASQ LALKPLVDGQLLNDQWPVINAVSGVSGAGRKAS MGNSFCEVSLQPYGLFTHRHQPEI VTHLGTPVIFTPHLGNFARGILATITCRLKAGVT AQNIADAYHHAYQNKPLVRLYQQG VPALKAVVGLPFCDIGFSVQGEHLIIVATEDNLL KGAAQAVQCMNIRFGFPETQSLL " </pre>
gene	334453..335229	/gene="argB"
CDS	334453..335229	<pre> /locus-tag="y0311" /gene="argB" /locus-tag="y0311" /function="enzyme; amino acid biosynthesis: Arginine" /note="residues 1 to 256 of 258 are 84.76 pct identical to residues 1 to 256 of 258 from E. coli K12 : B3959" /codon-start=1 /transl-table=11 /product="acetylglutamate kinase" /protein-id="AAM83902.1" /db-xref="GI:21956991" /translation="MMNPLVIKLGGVLLDSEEAL ERLFTALVTYREKHERPLVIMHGG GCLVDELMKRLALPVVKKNGLRVTPADQIDIITG ALAGTANKTLLAWAVKHQINAVGL CLADGNTVTVTLLDAELGHVGKAQPGSAALVQTL LAAGYMPIISSIGITVEGQLMNVN ADQAATALAATLGADLILLSDVSGILDGKGQRIA EMTAQKAEQLIAQGIITDGMVVKV NAALDAARSLGRPVDIASWRHSEQLPALFNGVPI GTRISV" </pre>
gene	335396..336769	/gene="argH"
CDS	335396..336769	<pre> /locus-tag="y0312" /gene="argH" /locus-tag="y0312" /function="enzyme; amino acid biosynthesis: Arginine" /note="residues 1 to 456 of 457 are 89.03 pct identical to residues 1 to 456 of 457 from E. coli K12 : B3960; residues 1 to 456 of 457 are 90.57 pct identical to residues 1 to 456 of 458 from GenPept : >gb AAL22962.1 (AE008892) argininosuccinate lyase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="argininosuccinate lyase" /protein-id="AAM83903.1" /db-xref="GI:21956992" /translation="MALWGGRFSQAADQRFKQFN DSLRFDYRLAEQDIIGSVAWSKAL VTVGVNLNADEQQQLEQALSVLLEEVQANPHAILA </pre>

		SDAEDIHSWVETKLIDKVGDLGKK LHTGRSRNDQVATDLKLWCKFQITELQTAVQQLQ QALVMTAEANQDAVMPGYTHLQRA QPVTFAHWCLAYVEMLSRDESRLQDTLKRLDVSP LGCGALAGTAYAIDREQLAGWLGF ASATRNSLDSVSDRDHVLELLSDASIGMVHLSRF AEDLIFFNSGEAAFVDLSDRVTS SSLMPQKKNPDALELIRGKCGRVQGALTGMTMTL KGLPLAYNKDMQEDKEGLFDALDT WLDCLHMAALVLDGIQVKRPRCKEAAEQGYANAT ELADYLVAKGVFPFREAHHIVGEAV VEAIRQGKALEALALSDLQQFSSVIGDDVYPILA LQSCLDKRVAKGGVSPQQVASAIA EAKARLF"
gene	337368..339860	/gene="hasR" /locus-tag="y0313"
CDS	337368..339860	/gene="hasR" /locus-tag="y0313" /function="transport: transport of small molecules; cations" /note="receptor for HasA and heme; residues 42 to 830 of 830 are 55.62 pct identical to residues 122 to 899 of 899 from GenPept : >emb CAA70172.1 (Y08983) hasR [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="putative outer membrane receptor" /protein-id="AAM83904.1" /db-xref="GI:21956993" /translation="MDNIIRDKKTIIISVNKITTC ILFALVTQGYSGQLAANTAETPTN NNDMALDKLNVEGKGNNAHSDWIYDEPRSVSEIT REQLDNRPARHAADILEQTPGVYS SVSQQDPGLSINIRGIQDYGRVNMNIDGMRQNF KSGHGQRNGSMYIDPEILSNVVIE RGIFNGIGGAGAIGGIATFNTINASDFLAPEKEL GGHIRAMTGDNGTRFIGSGALALG NPNGDILLAVSERNLKDYWPGNKGVLAGLRLYSP TRNVGDDLKNTKTLFTGYKMRSQ AKVGWNFEAGQRLEFSYLQTQIASPNASMLSEVL ALSPSGKEITKIGWRNTSFTNVEN RNIALDYRLNPEHISWLDATAKIYYVDTNDET ANSLFKEYFWTQTRLKTRGLQLQN TNTFTPSDAHQIRLKYGLEWFSKSEGYSTRKLI ERTTPPGKRAITSTFAQLNIEYDD WLRLEGLRYDQFRLKGNTWLHTRSFLQPYTFEN PCDRRIHEQSEKPGSRCSSRRPAT MRWDVDRCEQQLSPTLAMGVKPGLEWLEFFGSYG KSWRPPAMTEVLATGTAHGYSWVL PNPFVAAERARTWEAGFNIQQSNLFIEDDHFAAK VAYFDTRIANYINLELGKAKPKFG GDSFTDVAYVNNLLKTRFRGLEYSYDAGTFYT NINYTRMIGVNNVCSPYAWLGGLQ SVKYKYVGKVEQIYAVENEVANNYVTCMNANVLF GSSAYLPGDRGSLTLGSRIFDRRL DFGTVIRYNKGYQDRSAQDENGNP LTAYVADWPK YIVYDLYASYKVTNNLILRSSIEN ITNRAYLVNYGDTLSFAPSRGRTIQGGFEYKF"
gene	340082..340699	/gene="hasA" /locus-tag="y0314"

CDS	340082..340699	<pre> /gene="hasA" /locus-tag="y0314" /function="transport: transport of small molecules; cations" /note="secreted heme-binding protein experimentally shown to bind heme; residues 1 to 181 of 205 are 31.60 pct identical to residues 1 to 182 of 188 from GenPept : >emb CAA57068.1 (X81195) hasA [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="secreted hemophore" /protein-id="AAM83905.1" /db-xref="GI:21956995" /translation="MSTTIQYNSNYADYSISSYL REWANNFGDIDQAPAETKDRGSFS GSSTLFSGTQYAIGSSHSNPEGMIAEGDLKYSFM PQHTFHGQIDTLQFGKDLATNAGG PSAGKHLEKIDITFNELDLSGEFDSGKSMTENHQ GDMHKSVRGLMKGNPDPMLEVMKA KGINVDTAFKDLASQYPDSGYMSDAPMVDTVG VVDCHDMLLAA" </pre>
gene	340850..342673	<pre> /gene="hasD" </pre>
CDS	340850..342673	<pre> /locus-tag="y0315" /gene="hasD" /locus-tag="y0315" /function="transport: transport of small molecules; cations" /note="secretion of HasA; residues 22 to 589 of 607 are 62.14 pct identical to residues 1 to 566 of 582 from GenPept : >dbj BAA12015.1 (D83582) metalloprotease transporter [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="secretion ATPase, Type I secretion system" /protein-id="AAM83906.1" /db-xref="GI:21956996" /translation="MEMDAMESCKTPGASSVPPT ILSVLAGNKKILWGIGLFTAVINL LMLAPAIYMLQVYDRVLASANTMTLLMLTVLVLG VFVFIGLLEWVRSAVVIRLGTQID MQLNQPVFNAAFAANLKGHNTPAAQALNDLTVLR QFATGNALFAFFDAPWFPLYLLVI FLLHPWLGMLAAAGAGILVVLAWLNQWICKKPLH DASIITSHATQQANANLRNADVIE AMGMLKALRERWLMQHANFLYQQNLASDKSSRV TAVAKSSRQALQSMMLGLGALLVIY NEITAGVMIAGSILIGRVLGPIDQLIAVWKQWSH ARLAYQRLSQLLAQHPSSPTGMVL PAPQGKLNVTQLMACKPGTHIPVLHSINFELQPG DVLGILGPSGSGKSTLAKLLVASQ PTFSGTVRLDSADLSRWDKTQLGEFIGYLPQNIQ LFRGTVAENIARFGAIDTAKVVAA AQLADVHDLILHLPQGYDTPLGDDGEGLSGGQRQ RIALARAMYGIPRLIVLDEPDASL </pre>

gene	342749..344077	DKEGEQALLASIIQLKQQGCTIVMITHKPELLSG SDYLLFLKNGQMDLFDRTQAVLQN IQGKDKPAVQPEAKILNSRSGWSNGVSYGIGPAR TTSSPKP" /gene="hasE" /locus-tag="y0316"
CDS	342749..344077	/gene="hasE" /locus-tag="y0316" /function="transport: transport of small molecules; cations" /note="secretion of HasA; residues 20 to 442 of 442 are 47.54 pct identical to residues 17 to 443 of 443 from GenPept : >dbj BAA12016.1 (D83582) metalloprotease transporter [Serratia marcescens]" /codon-start=1 /transl-table=11 /product="secretion permease, Type I secretion system" /protein-id="AAM83907.1" /db-xref="GI:21956997" /translation="MLPESVCYSVANANRQPPLQ INSGRYLNIGGGLVVIGFIGFLLW AGLAPLDKGVAVTGLLVVAENRKVIQPLQGGRIQ QLHVTEGDEIVSGQLLVTLDDTAI RNQRDNLQHQYLSALAQEARLTAEQNDLDVITFP QALLEHATQPAVERNIIILQQQLLH HRRQAHLSEIARLSTQLTRHQARLDGLQAMRSNH QRQSNLFQQQLDSVQLLAKDGHIA KNKLLEMESQSTSLQARVEQSTSDIAEAHKLIDE TEQHVLRREQYQSENSEQLAKAQ QNTQELVQRLNIAEYELSHTRIFAPVSGSVIALA QHTVGGVVSSGQALMEIVPSGQPL FVEAQLPVELIDKVAVGLPVDLNFSAFNQSNTPR LQGSVWRIGADRIQPPPTSPPYYP LTVAILDLPTELAIRPGMAVDVFIRTGERSLLSY LFPFTDRLHLALAE" /gene="hasB" /locus-tag="y0317"
gene	344142..344945	/gene="hasB" /locus-tag="y0317"
CDS	344142..344945	/gene="hasB" /locus-tag="y0317" /function="transport: transport of small molecules; cations" /note="possibly specific for heme-HasA uptake via HasR receptor; residues 14 to 265 of 267 are 36.90 pct identical to residues 16 to 257 of 258 from GenPept : >gb AAK67308.1 (AF283294) CjrB [Shigella flexneri]" /codon-start=1 /transl-table=11 /product="TonB-like protein" /protein-id="AAM83908.1" /db-xref="GI:21956998" /translation="MNRLQQSSDKLIFWLVGALL ACGIHIYALWWLSTASIPAITYSY PAAIMMELSAEPEFMQNLPQNSVVGITQNIIEPA VEQRVNQPDIDVLDLPTLPEQPEGQ"

```

REITRKEPIKVKRPAENRATSRKPVNKETQESDS
KQSSPAAAASAMLSGTSQQVAAAV
NSDSSHRQQAQVSWKSRLQGHLMGFKRYPSSARK
QQQQGTAMIRFVVDKNGYVSSVQL
SHSSGTSALDREALAIKRAQPLPKPPAELLSQG
QITLSLPVDFNLKRK"
gene      complement(345061..3465 /locus-tag="y0318"
24)
CDS       complement(345061..3465 /locus-tag="y0318"
24)

/function="enzyme; oxidoreductase"
/note="residues 1 to 486 of 487
are 75.00 pct identical to
residues 1 to 483 of 484 from
GenPept : >gb|AAF95779.1|
(AE004330) pyridine
nucleotide-disulfide
oxidoreductase, class I [Vibrio
cholerae]"
/codon-start=1
/transl-table=11
/product="putative pyridine
nucleotide-disulphide
oxidoreductase"
/protein-id="AAM83909.1"
/db-xref="GI:21956999"
/translation="MKTLNVDVAVIGGGTAGLGA
YRAAKLLTPNVVMIEGGEYGTTC
RVGCMPSKLLIAAAEAVHQIEKAPGFGIHPQGKP
LINGREVM DRV K RERDRFVGVLE
SVETIPAADKIQGYARFIDDNTLQVDDHTQLTSQ
KIIAQRIVIATGSRPSWPASWNL
GDRLIINDDVFNWDDLPEVAVFGPGVIGLELGG
ALHRLGVQVKMFGVGGAVGPLTDS
IVRDYAAKTLGDEFYLDPDVKVELMQREGDKVFI
RYLDKSGRPQEIMVDYVLAATGR
PNVDKLGLENTSLILDERGV PQADRLTMQTNPVH
IFIAGDASNQLPLLHEASDQARIA
GVNAGGFPEVVPGLRRSPISVVFSDPQIAMVGAT
FRELAQKFSACGCFEIGEVSFENQ
GRSRVMLKNKGILRIYGEQGTGRFLGAEMMGPSA
EHIAHLLAWAHQQMTIDQMLDMP
FYHPVIEEGLRTALRDLQSKLKLGADEAERCLRC
PGE"
gene      complement(346619..3473 /locus-tag="y0319"
50)
CDS       complement(346619..3473 /locus-tag="y0319"
50)

/function="enzyme; oxidoreductase"
/note="residues 1 to 241 of 243
are 81.32 pct identical to
residues 5 to 245 of 247 from
GenPept : >gb|AAF95778.1|
(AE004330) peroxiredoxin family
protein/glutaredoxin [Vibrio
cholerae]"
/codon-start=1
/transl-table=11
/product="peroxiredoxin family
protein"
/protein-id="AAM83910.1"
/db-xref="GI:21957000"

```


		/translation="MFTSQEGKKVPQVTFHTRQG DQWIDVTDDLF SNKTVIVFSLPG AFTPTCSSSHLPRYNELAGVFKQHGVD SILCVSV NDTFVMNAWKSDQHAENITFVPDG NGEFTKGMNMLVEKADLGFGPRSWRYSMLVRNGV VEKMFVEPNKPGDPFEVSDADTML KYLAPDFKQESVAVFTKPGCPFCAKAKQMLQDH GLQYEEIVLGKDATTVSLRAVSGR STVPQIFIGGRHIGGSDDLEKYLPA"
gene	347497..348414	/gene="oxyR"
		/locus-tag="y0320"
CDS	347497..348414	/gene="oxyR"
		/locus-tag="y0320"
		/function="regulator; global regulatory functions"
		/note="residues 1 to 305 of 305 are 86.55 pct identical to residues 1 to 305 of 305 from E. coli K12 : B3961; residues 1 to 297 of 305 are 91.24 pct identical to residues 1 to 297 of 302 from GenPept : >gb AAC72241.1 (U74302) oxidative stress transcriptional regulator [Pectobacterium carotovorum]"
		/codon-start=1
		/transl-table=11
		/product="activator, hydrogen peroxide-inducible genes"
		/protein-id="AAM83911.1"
		/db-xref="GI:21957001"
		/translation="MNIRDLEYLVALAEFRHFRR AADSCHVSQPTLSGQIRKLEDELG IMLLERTSRKVLFTQAGLLLVEQAKTVLREVKVL KEMASLQGESMSGPLHIGLIPTVG PYLLPQIIPMLHKTFPKLEMYLHEAQTQNLLAQL DSGKLDCAILALVKETEAFIEIPL FDEPMNLAIYADHPWANRERVEMHELAGEKLLML EDGHCLRDQAMGFCFQAGADEDTH FRATSLETLRNMVAAGSGITLLPALAVPNRQRD GVCYLECYKVPVKRTIALVYRPGS PLRGRYEQLAEAIRDHMQERMAPSLEQAI"
gene	complement(348397..3497 31)	/gene="udhA"
		/locus-tag="y0321"
CDS	complement(348397..3497 31)	/gene="udhA"
		/locus-tag="y0321"
		/note="residues 1 to 444 of 444 are 84.00 pct identical to residues 1 to 444 of 444 from E. coli K12 : B3962; residues 1 to 444 of 444 are 85.36 pct identical to residues 23 to 466 of 466 from GenPept : >gb AAL22964.1 (AE008893) soluble pyridine nucleotide transhydrogenase [Salmonella typhimurium LT2]"
		/codon-start=1
		/transl-table=11
		/product="putative oxidoreductase"
		/protein-id="AAM83912.1"

		/db-xref="GI:21957002" /translation="MGLVKQGARVAVIERYNVVG GGCTHWGTIPSKALRHAVSRIIEF NQNPPLYSDNARTIKSSFADILNHADRVINQQTRM RQGFYDRNHCHMFSGDASFIDANT VNVRYADGTSDDLQADNIVIATGSRPYRPVNVDF NHERIYDSDTILQLSHEPQHVIY GAGVIGCEYASIFRGLSVKVDLINTRDLLAFLD QEMSDALSYHFWNNGVVIRHNEEF EQIEGTTDGVIVHLKSGKKVKADCLLYANGRTGN TSGLGLENIGLEADSRGLLKVNSM YQTALSHVYAVGDVIGYPSLASAAYDQGRIAAQA MIKGEANVHLIEDIPTGIYTIPEI SSVGKTEQELTAMKVPYEVGRAQFKHLARAQIVG MDTGSLKILFHRETKQILGIHCFG ERAAEIIHIGQAIMEQKGEGNTLEYFVNTTFNYP TMAEAYRVAALNGLNRLF"
gene	350003..350650	/locus-tag="y0322"
CDS	350003..350650	/locus-tag="y0322" /note="residues 4 to 210 of 215 are 95.65 pct identical to residues 19 to 225 of 234 from E. coli K12 : B3963" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83913.1" /db-xref="GI:21957004" /translation="MGTIMGVRAQQKERTRRSLI EAAFSQLSAERSFASLSLREVSRE AGIAPTSFYRHF RDVDELGLTMVDESGLMLRQLM RQARQRIAKGGSVIRTSVSTFMEF IGNNPNAFRLLLRRERSGTSAAFRAAVAREIQHFI AELADYLELENHMPRSFTEAQAEA MVTIVFSAGAEVLDVDIEQRRQLEERLVLQLRMI SKGAYYWYRREQEKLASRVE"
gene	350663..351070	/locus-tag="y0323"
CDS	350663..351070	/locus-tag="y0323" /note="residues 3 to 115 of 135 are 66.37 pct identical to residues 2 to 114 of 119 from E. coli K12 : B3964; residues 3 to 115 of 135 are 70.79 pct identical to residues 2 to 114 of 119 from GenPept : >gb AAL22966.1 (AE008893) putative inner membrane protein [Salmonella typhimurium LT2]"
gene	complement (351204..352307)	/codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83914.1" /db-xref="GI:21957005" /translation="MEQSSRRETGTLALLALITGL AINGVCAALFSALVPFVSFPLLT ILAVYCLHQRYLNFAMPQGIPVLASACFLLGILL YSAIVRVEYPAIGSNFVPAVLSVV LVFWILFKLRTRKSVQTHTDADIDINNSDQPQQ"
		/gene="trmA"
		/locus-tag="y0324"
CDS	complement (351204..352307)	/gene="trmA"

07)

gene 352703..354664
CDS 352703..354664

```
/locus-tag="y0324"  
/function="enzyme; aminoacyl tRNA  
synthetases, tRNA modification"  
/note="residues 1 to 363 of 367  
are 77.41 pct identical to  
residues 1 to 363 of 366 from E.  
coli K12 : B3965; residues 1 to  
363 of 367 are 77.41 pct identical  
to residues 1 to 363 of 366 from  
GenPept :  
>gb|AAG59169.1|AE005628-5  
(AE005628) tRNA  
(uracil-5-)-methyltransferase  
[Escherichia coli O157:H7 EDL933]"  
/codon-start=1  
/transl-table=11  
/product="tRNA  
(uracil-5-)-methyltransferase"  
/protein-id="AAM83915.1"  
/db-xref="GI:21957006"  
/translation="MTPNILPIESYDHLAEKSA  
RLKAMMLPFQAPEPEIFRSPADHY  
RMRAEFRVWHEDDLYHIMFDQQTQIRVEQFP  
VASRLINRLMDALMTAIRAEPLLR  
RKLFQIDYLSLTSGLIASLLYHRQLDEEWQKA  
LELRDQLRAQGFDLQLIGRAAKTK  
IMLDHDYIDEVLPVAGREMIYRQVENSFTQPNAA  
VNIHMLEWALDVTQGATGDLLLEY  
CGNGNFSLALARNFERVLATEIAKPSVAAAQYNI  
AANNIDNVQIIRMSAEFTQAMQG  
VREFNRLKGIDLGSYNCEITFVDPFRSGLDHETV  
KLVQAYPRILYISCNPETLCANLE  
QLQHTHKISRLALFDQFPYTHMECGVLLEKRH"  
/gene="btuB"  
/locus-tag="y0325"  
/gene="btuB"  
/locus-tag="y0325"  
/function="membrane; outer  
membrane constituents"  
/note="residues 31 to 653 of 653  
are 64.84 pct identical to  
residues 2 to 614 of 614 from E.  
coli K12 : B3966"  
/codon-start=1  
/transl-table=11  
/product="outer membrane receptor  
for transport of vitamin B12, E  
colicins, and bacteriophage BF23"  
/protein-id="AAM83916.1"  
/db-xref="GI:21957007"  
/translation="MAVAYYRPWHCGIRQLSLDA  
LLMIKNTMTIKKYTLTALSUTA  
FSGWAQGNNTTDNDEMVTANRFPQPKSSVLAP  
VDVVTRADIDRWQSTNINDVLRRL  
PGVDIAQDGGMGQRSSLFIRGTNSSHVLVLIDGV  
RLNQAGITGASDLSQIPISLVQRI  
EYIRGPRSAVYGSDAIGGVINILTGRDKPGTTLS  
AGLGSNGYQTYDGSTQQKLGEDTT  
VTLAGNYTYSKGYDVVAGMPGAGGPRQPDRDGM  
GKMLWAGLEHQFNEQFNGFARVYG  
FDNRSDYDGYTNYSNPLALIDTRKLSRITYDTGL
```

		RYKNGIYASQFIASYNRTKDYNYS PLFGQHDITASLDEAEQYNLQWGNTFQLTNGMIS AGADWQEQRTERKSSNQNTTADFT QHNTGIYLTGQQQISDVTLEGAVRSDDNSQFGWH STWQTSAGWEFIDGYRLIGSYGTA YKAPNLMQLYSAYGGNANLKPEESKQWEGGVEGL TGPLTWRLSAYRNDIDQLIDYSNL TNGYFNINKATIKGVEWTGSFDTGPLSHQVTLEY LDPRNADTHEILVRRAKQQVKYQL DWQVADLDWSVTYQYLGQRYDKDYSTYPEETVEL GGVSLWDLAVSYPVTSHLTVRGRI ANLFDKDYEMVYGYQTPGREYYFTGSYNF"
gene	354573..355472	/gene="murI"
CDS	354573..355472	/locus-tag="y0326" /gene="murI" /locus-tag="y0326" /function="enzyme; murein sacculus, peptidoglycan" /note="required for biosynthesis of D-glutamate and peptidoglycan; residues 9 to 299 of 299 are 71.13 pct identical to residues 1 to 287 of 289 from E. coli K12 : B3967; residues 13 to 299 of 299 are 73.17 pct identical to residues 1 to 283 of 283 from GenPept : >gb AAL22969.1 (AE008893) glutamate racemase [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="glutamate racemase" /protein-id="AAM83917.1" /db-xref="GI:21957008" /translation="MPTCLIKIMRWFMATKPQDA NTTSREAITSKADSPPRPTALIFD SGVGGLSVYQEIRQLLPDLHYIYAFDNVAFPYGE KSGEFIVERVLEIVTAVQQRHPLA IVVIACNTASTVSLPALRERFAFPVVGVPVPAIKP AVRLTRNGVVGLLATRATVHASYT LDLIARFATDCKIELLGSSSELVEVAETKLHGGVV PLEVLKKILHPWLSMREPPDTIVL GCTHFPLLTEELAQVLPEGTRMVDSGAARIARRTA WLISSQENVISSQDENIAYCMALD EDTDALLPVLQSYGFPKLQKLPI"
gene	355930..357514	/locus-tag="yr005"
rRNA	355930..357514	/locus-tag="yr005" /product="16S ribosomal RNA"
gene	357608..357680	/locus-tag="yt003"
tRNA	357608..357680	/locus-tag="yt003" /product="tRNA-Glu" /note="anticodon: TTC"
gene	357936..360842	/locus-tag="yr006"
rRNA	357936..360842	/locus-tag="yr006" /product="23S ribosomal RNA"
gene	complement(360878..361270)	/locus-tag="y0327"
CDS	complement(360878..361270)	/locus-tag="y0327" /note="residues 5 to 36 of 130 are 50.00 pct identical to residues 11 to 48 of 50 from GenPept :

		>emb CAB67146.1 (AJ271079)
		hypothetical protein [Oenothera
		elata subsp. hookeri]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83918.1"
		/db-xref="GI:21957009"
		/translation="MAERTGLEPATPCVTGRYSN
		QLNYRSTDSFTCIFPILYPIRASA
		LRCAKPLLAITVTRCHSDNSCLMPGSVLLSHGE
		TPHYHRRYGVSLSSAWDQVGPPR
		YGRQANSVLINPQTSNTCQPVNTISERR"
gene	360950..361069	/locus-tag="yr007"
rRNA	360950..361069	/locus-tag="yr007"
		/product="5S ribosomal RNA"
gene	361193..361272	/locus-tag="yt004"
tRNA	361193..361272	/locus-tag="yt004"
		/product="tRNA-Asp"
		/note="anticodon: GTC"
gene	361278..361350	/locus-tag="yt005"
tRNA	361278..361350	/locus-tag="yt005"
		/product="tRNA-Trp"
		/note="anticodon: CCA"
gene	362330..363286	/locus-tag="y0328"
CDS	362330..363286	/locus-tag="y0328"
		/function="putative regulator"
		/note="residues 1 to 318 of 318
		are 75.78 pct identical to
		residues 1 to 318 of 318 from E.
		coli K12 : B4227"
		/codon-start=1
		/transl-table=11
		/product="solute-binding
		periplasmic protein of ABC
		transporter"
		/protein-id="AAM83919.1"
		/db-xref="GI:21957011"
		/translation="MYRRLLLAAAVTAAMCSAVQ
		AAPLVVGFSQIGSESGWRSATKV
		AKQEAEKRGITLKIADAQQKQENQIKAVRSFIAQ
		GVDAIFIAPVVATGWTPVLQEAKE
		AKIPVFLLDRMIEVNDPSLYTAAVASDSVYEGKV
		AGEWLLQDVAGKPCNVVELQGTVG
		SSVAINRKKGFADGIASAPGVKIIIRSQSGDFTRS
		KGKEVMESFIKAEQNGKNICAVYA
		HNDDMAIGAIQAIKEAGLKPGSDIKIVSIDGVPD
		IFKAMSSGEANATVELTPNMAGPA
		LDALIVLKKDGTQPPKFIQTESRLLQPD TAKQEY
		ELKKSLGY"
gene	363372..364862	/locus-tag="y0329"
CDS	363372..364862	/locus-tag="y0329"
		/function="putative transport"
		/note="residues 4 to 376 of 496
		are 62.73 pct identical to
		residues 9 to 381 of 417 from E.
		coli K12 : B4228; residues 4 to
		494 of 496 are 67.20 pct identical
		to residues 9 to 499 of 500 from
		GenPept :
		>gb AAG59426.1 AE005655-5
		(AE005655) putative ATP-binding

		component of ABC transporter [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative ATP-binding component of ATP transport system" /protein-id="AAM83920.1" /db-xref="GI:21957012" /translation="MEILLEVRGLSVEFPGVKAL DSVDFSLQRGEVVALLGENGAGKS TLIKALTGVYKRSAGEVLLDGKAVCPIDTADAQL MGIGTVYQEVNLLPNISVAANLFI GREPLRWGLIDHNKMNQQAALLTGyGLTLDVQQ PLANFSIAIQQIVAIARAVDLSAK VLILDEPTASLDAKEVSMLLDILCQLRDQGIGMV FVTHFLDQVYRISDRITVLRNGKL VGTKTVAELPRIELVQMMLGHSFDEQLLRGEHS ITNKNPLVEFKNYGRRGVVENFDL SVSPGEIVGLAGLLGSGRTETAQLIFGITTPDTG EAKIQGKPKVIRTTPRKASKFGFGY CPEDRKTEGIVGAATVRENIILALQAQRGWLRLPL SMREQTQIADDFIQQLGIRTPSPE QQIQYLSGGNQQKVLLARWLATKPRFLILDEPTR GIDVGAHAEEIRLIEKLCDEGLAL LIISSELEELAGYADRIIVLRDRRHVAQLDHDEI SVPAIMQAIQVQ" /locus-tag="y0330" /locus-tag="y0330" /function="putative transport" /note="residues 4 to 326 of 339 are 70.67 pct identical to residues 4 to 325 of 341 from E. coli K12 : B4230; residues 4 to 326 of 339 are 70.37 pct identical to residues 4 to 325 of 341 from GenPept : >gb AAG59427.1 AE005655-6 (AE005655) putative transport system permease protein [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative ABC transport system inner membrane permease protein" /protein-id="AAM83921.1" /db-xref="GI:21957013" /translation="MGNRSLSMTQRPRKVWVLP KGATQFGALAVILLIDSLVAPHFF SIHIQDGRFLFGSIIDILNRGAPVALLALGMTLVI ATGGIDLSVGAVMAIAGATAATLT SAGYPFMTVLALSLAVGALCGLWNGFLVAVLQIQ PIVATLMLMVAGRGIAQLITEGQI VTFDSGGLATLGSSTLMLPMSVVIACSMILILVW LLTRKTALGLFIESVGINLRSARN AGVSTRVLVIAVYVICGVCAAVAGIIVTADIRGA DANNAGLWLELDAILAVVIGGASL MGGRFNLLLSVIGALIIQGMNTGILLSGYQPEFN LVLKAIVVLAVLVVQSPMISLSHL FQRRK" /locus-tag="y0331" /locus-tag="y0331" /function="putative transport"
gene	364874..365893	
CDS	364874..365893	
gene	365893..366885	
CDS	365893..366885	

		<pre> /note="residues 9 to 330 of 330 are 70.18 pct identical to residues 1 to 318 of 323 from E. coli K12 : B4231" /codon-start=1 /transl-table=11 /product="putative ABC transporter permease protein" /protein-id="AAM83922.1" /db-xref="GI:21957014" /translation="MLKRVPLLLITIAVFILGYA FCLSQFPSFSSSRVWCDLLTDNAF LGIVAVGMTFVILSGGIDLSVGSVIAFTGVLLAK LIGTYGIHPVYAFAIVLVMGAMFG ALMGWIIDSLKLPAFIITLAGMFFIRGMSFIVSE ESLPINHPIYETLANYAWRVPGGG RFTLLAFIMLMVVAFGILLAHHTRFGHNVYAIGG NSVSAGLMGVPVRRTTIKIYMLSS TLAALSGIVFSLYTSAGYALAASGVELDAIAAVV IGGTLLAGGIGTVFGTLFGVLIQG LIQSYITFDGTLSSWWTKIVIGILLFSFIVIQKA MSAFYLNRRSRPQSSPLTPV" </pre>
gene	complement(366872..3677	/locus-tag="y0332"
	53)	
CDS	complement(366872..3677	/locus-tag="y0332"
	53)	
		<pre> /note="residues 84 to 280 of 293 are 50.99 pct identical to residues 3 to 190 of 198 from E. coli K12 : B3762; residues 1 to 281 of 293 are 62.32 pct identical to residues 1 to 272 of 278 from GenPept : >emb CAD09467.1 (AL627279) possible LysR-family transcriptional regulatory protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83923.1" /db-xref="GI:21957015" /translation="MDTELLKTFLEVSRTTRHFGR AAESLYLTQSAVSFRIRQLENQLG ANLFTRHRNNIIRLTPAGERLVPYAEMLLNTWRLA KKEVIHSLQHTELSIGATASLWEA YLTPWLQQLYEQQEELRLEARIALRNSLVKQLHE RQLDLLITTEPPKMDELACLLLGH FSLRLYSSFSLDLPKEDDTPNEHKNASEVPYIKL EWGADFHQQENRLLDSEQAPILTT TSAHLTRQLLETTGGCAFLPEHWQKEYPQLVIHP DIPPIVRPLYAVWLQNSDQQALIR QLLKTPMNNATQSVTRE" </pre>
gene	367788..368210	/locus-tag="y0333"
CDS	367788..368210	/locus-tag="y0333"
		<pre> /note="residues 29 to 140 of 140 are 83.03 pct identical to residues 1 to 112 of 112 from E. coli K12 : B3764" /codon-start=1 /transl-table=11 /product="hypothetical protein" </pre>

		/protein-id="AAM83924.1" /db-xref="GI:21957016" /translation="MFCFTRCQAYLILRAINSTT MRELGACQMADSFITTNRFFDNKH YPRGFSRHGDFTIKEAQLLERHGYAFNELDSGKR EPVTEEEQRFVAVCRGEREPVSAE EKVWSKYVIRTRQPKRFHTLSGGKPQMDAVEDYT DSDD"
gene	complement(368467..3700 11)	/locus-tag="y0334"
CDS	complement(368467..3700 11)	/locus-tag="y0334"
		/function="putative regulator" /note="residues 1 to 513 of 514 are 62.76 pct identical to residues 4 to 515 of 516 from E. coli K12 : B3765" /codon-start=1 /transl-table=11 /product="putative 2-component regulator" /protein-id="AAM83925.1" /db-xref="GI:21957017" /translation="MTAKESIMSLATIHTRATLG IQAPPVAVEVHISNGLPGLILVGL PETTVKEARDRVR SALINSGFNFPKRITVSLAP ADLPKEGGRYDLPIALAILAASEQ IPADKLAHYEFLGELALSGALRRVSGAIPAALTC SEANRQLILPTANGLEIGLIPQGN SWVADHLLAVCGFLQGENPLAQGQPFEPAPSPDN HLDLHDIIGQSQAKRALEIAAAGG HNLLLLGPPGTGKTM LATRLTG LPLTDQEAL AAAITG LLHSNALPTQWRCRAFRA PHHSASMAALIGGGSIPRPGEISLAHNGVFLDE LPEFERRVLD SLREPLESGEIIIS RAAAKICFPKVQLIAAMNPSPSGHYQGVHNRT PQQILRYLAKLSGPFLDRFDLSIE VPLLPA GMLGAQKNQGE SATVKQ RVLQARQ RQM DRAGKINTQLTSQEVAEFCYLAPE DAAFLEQVLLTLGLSVRAWHHILKVARTIADLAQ EKTIQKSHLSEALSYRCMDRLLLQ LHKSLM"
gene	370374..370472	/gene="ilvL"
		/locus-tag="y0335"
CDS	370374..370472	/gene="ilvL"
		/locus-tag="y0335" /function="leader; amino acid biosynthesis: Isoleucine, Valine" /note="residues 1 to 32 of 32 are 81.25 pct identical to residues 1 to 32 of 32 from E. coli K12 : B3766" /codon-start=1 /transl-table=11 /product="ilvGEDA operon leader peptide" /protein-id="AAM83926.1" /db-xref="GI:21957018" /translation="MKAILQVINLV LISVVV IIPCGAALGRRKA"
gene	370613..372259	/gene="ilvG"
		/locus-tag="y0336"
CDS	370613..372259	/gene="ilvG"

		/locus-tag="y0336" /function="enzyme; amino acid biosynthesis" /note="residues 1 to 548 of 548 are 79.92 pct identical to residues 1 to 548 of 548 from GenPept : >gb AAG58963.1 AE005608-4 (AE005608) acetohydroxy acid synthase II [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="acetohydroxy acid synthase II" /protein-id="AAM83927.1" /db-xref="GI:21957019" /translation="MNGAQWVVQALRAQGVDTVF GYPGGAIMPVYDALYDGGVEHLLC RHEQGAAIAAIGYARATGKVGVCIAITSGPGATNL ITGLADALLDSVPVIAITGQVGSA LIGTDAFQEIDVLGLSLACTKHSFLVESLDALPE IMAEAFAIATSGRPGPVLIDIPKD IQLAVGELTPHLKPVEEHSVDSAAELQHAWDMLA NAQKPMLYVGGGVGMAQAVPALRD FIAMTGIPAVATLKGLGAPDIAHPCYLGMLGMHG TKAANFAVQDCDLLVAVGARFDDR VTGKLNTFASKAKVIHMDIDPAELGKLRQVHVAL QGNLNVLLPALQQPLNIQSWRDEV MALKQQHHWRYDHPGQAIYAPLLLLKQISERKAPE TVVTTDVGQHQMWTAQHMFTRPE NFITSSGLGTMGFGVPAAVGAQMARPDDMVICVS GDGSFMMNVQELGTIKRKQLPLKI VLLDNQRLGMVRQWQQLFFDGRYSETNLSDNPDF ITLASAFDIPGQRITRKDQVDAAL DALFNSEGPYLLQVSIDELENVWPLVPPGAGNET MLEKIS" /gene="ilvE" /locus-tag="y0337" /gene="ilvE" /locus-tag="y0337" /function="enzyme; amino acid biosynthesis: Isoleucine, Valine" /note="residues 27 to 332 of 333 are 91.17 pct identical to residues 3 to 308 of 309 from E. coli K12 : B3770; residues 27 to 332 of 333 are 91.50 pct identical to residues 3 to 308 of 309 from GenPept : >gb AAG58965.1 AE005608-6 (AE005608) branched-chain amino-acid aminotransferase [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="branched-chain amino-acid aminotransferase" /protein-id="AAM83928.1" /db-xref="GI:21957021" /translation="MSPVSRSYNLIHYRYAPDAP EGKKRMTKKADYIWFNGEMVPWAE
gene	372461..373462	
CDS	372461..373462	

gene	373725..375623	AKVHVMSHALHYGTSVFEGVRCYESHKGPVVFRRH REHMQRRLHDSAKIYRMPVSQSVDE LMEACRATLRKNNLTSAYIRPLVFIGDVGMGVNP PEGYN TDVIIA AFWGAYLGAEAL EQGIDAMVSSWNRVAPNTIPTAAKAGGNYLSSLL VGSEARRHGYQEGIALDVHGYLSE GAGENLFEVKDGILFTPPFTSSALPGITRD AIIK LAKDMGLEVREQVLSRESLYLADE VFMSGTAAEITPVRSVDGIQVGIGKRGPVTA KIQ QAFFGLFTGETEDKWGWLDQVNP" /gene="ilvD" /locus-tag="y0338"
CDS	373725..375623	/gene="ilvD" /locus-tag="y0338" /function="enzyme; amino acid biosynthesis: Isoleucine, Valine" /note="residues 37 to 632 of 632 are 86.04 pct identical to residues 4 to 605 of 605 from E. coli K12 : B3771" /codon-start=1 /transl-table=11 /product="dihydroxyacid dehydratase" /protein-id="AAM83929.1" /db-xref="GI:21957022" /translation="MRQTLICKIKTRSEETMPKY RSHTTTTHGRNMAGARALWRATGMT DDDFGKPIIAVVNSFTQFVPGHVHLRDLGKLVAE QIVASGGVAKEFN TIAVDDGIAMG HGGMLYSLPSRELIADSVEYMVNAHCADAMVCIS NCDKITPGMLMASLRLNIPVIFVS GGPMEAGKTKLSDKIIKLDLIDAMIQGANPNVSD EESAQIERSACPTCGSCSGMFTAN SMNCLNEALGLALPGNGSLLATHADRKQLFLDAG KHIVALTKRYYEQDDVSALPRNIA NKA AFENAMILD IAMGGSTNTVLHLLAA AQEGEI DFSMTDIDHLSRKVPHLCKVAPST QKYHMEDVHRAGGVIGILGELDRAGLLNRDVS NV LGLNLTQTLEAYDVMLTQDEGVKQ MYAAGPAGIRTTKAFSQDCRYPSLDTDREEGCIR TREHAYSQDGG LAVLYGNIAADGC IVKTAGVDKDSLTFRGP AKVFESQDEAVEAILGG KVVAGDVVVIRYEGPKGGPGMQEM LYPTTYLKSMGLGKSCALLTDGRFSGGTSGLSIG HVSPEAASGGLIGLVQDGDFINID IPNRGIVLDVSEAELAARRETEEAHGDAAWSPKG RERQVSYALRAYAMLATSADKGAV RDKSKLGG" /gene="ilvA" /locus-tag="y0339"
gene	375629..377173	/gene="ilvA" /locus-tag="y0339"
CDS	375629..377173	/gene="ilvA" /locus-tag="y0339" /function="enzyme; amino acid biosynthesis: Isoleucine, Valine" /note="residues 1 to 514 of 514 are 84.63 pct identical to residues 1 to 514 of 514 from E. coli K12 : B3772; residues 1 to 514 of 514 are 85.01 pct identical to residues 1 to 514 of 514 from GenPept : >dbj BAB38129.1 (AP002566) threonine deaminase

```

[Escherichia coli O157:H7]"
/codon-start=1
/transl-table=11
/product="threonine deaminase
(dehydratase)"
/protein-id="AAM83930.1"
/db-xref="GI:21957023"
/translation="MAVSQPLSAAPCGAEYLRAI
LRAPVYEVAQVTPQLQVMEKISSRV
GNTVLVKREDRQPVHSFKLRGAYAMISLTEEQK
ACGVVTASAGNHAQGVALSAHKMG
IKALIVMPVATADIKVDAVRAFGGEVLLFGANFD
EAKTKAIALAQEQGYTFVPPFDHP
AVIAGQGT LAMELLQQDAHLDRVFPVGGGGLVA
GVAVLIKQLMPQIKVIGVEAEDSA
CLRAALDAGQPVDLARVGLFAEGVAVKRIGDEPF
RLCQEYLDDVITVDSDAICAAVKD
LFEDVRAIAEP SGALALAGLKKYVQQHNIQGERL
AHVLSGANVNFHGLRYVSERCELG
EQREAL LAVTIPEQKGSFLRFCELLGGRSVTEFN
YRYADAENACIFVGVRLTRGYAER
VEILAELQDKGYQVVDLSDDMAKLHVRYMVGGR
PSKPLRERLFSFEFPESPGALLKF
LHTLGTHWNISLFHYRSHGTDFGRVLA AFELSAT
EPQFEERLAALGYCHDETDPAF KFFLAG"
gene      complement(377304..3777 /locus-tag="y0340"
89)
CDS       complement(377304..3777 /locus-tag="y0340"
89)
/notes="residues 7 to 161 of 161
are 33.72 pct identical to
residues 6 to 167 of 176 from
GenPept : >emb|CAD02952.1|
(AL627277) putative exported
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83931.1"
/db-xref="GI:21957024"
/translation="MRLPGAVMKAKSKKIICALL
LLGSILLGYFFWLSRHPVEIISVH
QRNNYS DILVRNFPFTEKGKINWWLENRDMLKAK
YSIPKPASDGFYTIIFWDFGDGYK
EEGKYDRLCFSDMNTTKNCIEKEKYMTIYKIKND
EPLFSFDGNRYFLNENNKIVKMKR E"
gene      complement(377848..3783 /locus-tag="y0341"
30)
CDS       complement(377848..3783 /locus-tag="y0341"
30)
/notes="residues 7 to 153 of 160
are 37.01 pct identical to
residues 6 to 152 of 176 from
GenPept : >emb|CAD02952.1|
(AL627277) putative exported
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM83932.1"

```

```

        /db-xref="GI:21957025"
        /translation="MRLPGAVMKAKSKKIICALL
        LLGSILLGYFFWLSLRPVEIVAIH
        KDGNFSAVLVRDFPVTDKGKINWWLENKSRLKDK
        YNIPNPAPDGGFFSITIWFDFGDGYK
        EEGKYDRRCFEDMKTSKNCIDKNSLMIIRNSQYN
        VMSFTLDSGIYQLKNGEIVKMKRE "
gene      complement(378389..3788 /locus-tag="y0342"
50)
CDS       complement(378389..3788 /locus-tag="y0342"
50)
        /note="residues 5 to 146 of 153
        are 39.35 pct identical to
        residues 8 to 152 of 176 from
        GenPept : >emb|CAD02952.1|
        (AL627277) putative exported
        protein [Salmonella enterica
        subsp. enterica serovar Typhi]"
        /codon-start=1
        /transl-table=11
        /product="hypothetical"
        /protein-id="AAM83933.1"
        /db-xref="GI:21957026"
        /translation="MKAKSKKTLYALLLIGSVLL
        GYFFWLSLRPVEIVAVHKDRNFSA
        VLVRDFPVTDKGKINWWLENKSRLKDKYNIPNPA
        PDGFFSITIWFDFGDGYKEEGKYDR
        RCFEDMKTSKNCIDKNSLMIIRNSQYNVMSFTLD
        SGIYQLKNGEIVKMKHE"
gene      complement(378834..3797 /locus-tag="y0343"
89)
        /note="disrupted by frameshift"
        /pseudo
gene      complement(380665..3815 /gene="ilvY"
49)
        /locus-tag="y0344"
CDS       complement(380665..3815 /gene="ilvY"
49)
        /locus-tag="y0344"
        /function="regulator; amino acid
        biosynthesis: Isoleucine, Valine"
        /note="residues 2 to 294 of 294
        are 73.72 pct identical to
        residues 1 to 293 of 297 from E.
        coli K12 : B3773; residues 2 to
        294 of 294 are 74.06 pct identical
        to residues 1 to 293 of 297 from
        GenPept :
        >gb|AAG58968.1|AE005608-9
        (AE005608) positive regulator for
        ilvC [Escherichia coli O157:H7
        EDL933]"
        /codon-start=1
        /transl-table=11
        /product="positive regulator for
        ilvC"
        /protein-id="AAM83934.1"
        /db-xref="GI:21957027"
        /translation="MMDLRDLKVFLHLAESRHFG
        RSAKAMHVSPSTLSRQIQRLIETI
        GQPLFLRDNRTVQLTDAGNQLKAFAQQTLLQYQQ
        LLHALGQHGPSLSGELRLFCSVTA

```

		AYSHLPPILDRFRARHPLVEIKLTTGDAADAVNK VQSNEADLGIAGRPEVLPTSVAFT QIGEIPLVLIAPALPCAVRSQVAVEKPDWAMIPF ILPEHGSPSRKRIDLWFRRQRITNP LIYATVSGHEAIVSMVALGCGVALIPSVVVDNSP EPVRNRISLLDDVSLVEPFELGVC VPKKRLQEPLIDAFWGLL"
gene	381832..383310	/gene="ilvC" /locus-tag="y0345"
CDS	381832..383310	/gene="ilvC" /locus-tag="y0345" /function="enzyme; amino acid biosynthesis: Isoleucine, Valine" /note="residues 1 to 492 of 492 are 92.07 pct identical to residues 1 to 491 of 491 from E. coli K12 : B3774; residues 1 to 492 of 492 are 92.27 pct identical to residues 1 to 491 of 491 from GenPept : >emb CAD09408.1 (AL627279) ketol-acid reductoisomerase [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="ketol-acid reductoisomerase" /protein-id="AAM83935.1" /db-xref="GI:21957028" /translation="MANYFNTLNLRRQQLAQLGKC RFMARDEFADAEAGYLKGKKVVIVG CGAQGLNQGLNMRDSDLVAYALRKEAIAEKRAS WRKATENGFKVGTYEELIPQADLV VNLTPDKQHSVVKAVQPLMKEGAALGYSHGFNI VEVGEQVRKDITVVMVAPKCPGTE VREEYKRGFGVPTLIAVHPENDPKGEGMAIAKAW AAATGGHRAGVLEFSFVAEVKSDL MGEQTILCGMLQAGSLLCFDKLVSEGTDAAAYAEK LIQFGWETITEALKQGGITLMMDR LSNPAKLRAYALSEQKEIMAPLFQKHMDDIISG AFSSGMMADWANDDVKLLNWREET GRTAFENAPQFEGKISEQEYFDHGVLMIAMVKAG VELAFETMVDSGIIIESAYYESLH ELPLIANTIAKRRLYEMNVVISDTAEYGNLYLFAN AAVPLLKEKFMDSLQAGDLGKSIP GSAVDNAQLRDVNEAIRNHPIEAVGHKLRGYMTD MKRIAVAG"
gene	383491..383691	/locus-tag="y0346"
CDS	383491..383691	/locus-tag="y0346" /note="residues 15 to 60 of 66 are 34.78 pct identical to residues 525 to 567 of 612 from GenPept : >gb AAL32622.1 (AY062544) Phospholipase like protein [Arabidopsis thaliana]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83936.1" /db-xref="GI:21957030" /translation="MLYYEPEFLGSLRQEAYNTY"

gene	383887..385329	EIAKTEREVAERNRVQKKPFGLFI
CDS	383887..385329	EEMTLQKTLTDSQVAETAHHII" /locus-tag="y0347" /locus-tag="y0347" /note="residues 340 to 454 of 480 are 44.16 pct identical to residues 257 to 376 of 386 from GenPept : >emb CAD16923.1 (AL646075) probable transmembrane protein [Ralstonia solanacearum]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83937.1" /db-xref="GI:21957031" /translation="MGLLMQQQRVNADLETAKIT EPQRVENARLTAEAAEKAARDRI SEEIAATEAKRQRMENERLAEQERQRVGTEKQV SEASCAQQASAWQNRFTLPALQPS GSAQYSFAASGMSAVGEAAELHNSFLAAQEQLSA IATISASGSVAAMIALGIYQTKVG ESSERPPGWNVSPKFVGSISLSAMGLPATESLAS QGEMALPVRMRIIDAKDWIGCTEI YAVKTGVAGVLPKVKVGAAQYDESTGVYTFITDS TPPRTLIFTPAQPPGAETRPILAP PGSTPATLQHTGEMIIPVITPTILPLPLYARD FHDYIIWFPADSGLEPVVYVYLNPS YGKTTAKGKYSGRDFNPDKAGGPIKNLDWKEIKI RGEVDEVKLVHTRRFGELEDNKL IERLEKILTNKLTATDIDKRFYTHEIRELERYRM LGIPDDVNDKSVWNAHTATLEDF KINEKTQPLYTSEAEDAYIKAELKNSLGSK"
gene	complement (386990..387808)	/locus-tag="y0348"
CDS	complement (386990..387808)	/locus-tag="y0348" /function="putative factor; folding and ushering proteins: Chaperones" /note="pili assembly; residues 42 to 262 of 272 are 46.46 pct identical to residues 7 to 227 of 237 from GenPept : >gb AAG05520.1 AE004640-9 (AE004640) probable pili assembly chaperone [Pseudomonas aeruginosa]" /codon-start=1 /transl-table=11 /product="putative pilus chaperone, PapD family" /protein-id="AAM83938.1" /db-xref="GI:21957032" /translation="MHMRKWLSVSNIMLSRINR RLRGLLLMTTCRVLTLPALTIGV LIMSALATSAVASVIAERTRIVFSEGSTEESLQL VNSNSYPVAVQVWVDDGNLMATPD KAVSPILVLPPVFRLQPQAQRSLRLILSGGSKLP ADRESAFWLNIYEIPKATPKSGD ESFVTLALRMQYKVFYRPNLPAPGDILGKALTF SLERNGDSALIKVNNPTPYASFA ALTIGSAEGPPEMVAPFSQLDFPLNRAPISDNKT"

gene complement(387774..3889 /locus-tag="y0349"
 46)
 CDS complement(387774..3889 /locus-tag="y0349"
 46)
 /note="residues 2 to 390 of 390
 are 45.88 pct identical to
 residues 56 to 453 of 453 from
 GenPept :
 >gb|AAG05519.1|AE004640-8
 (AE004640) hypothetical protein
 [Pseudomonas aeruginosa]"
 /codon-start=1
 /transl-table=11
 /product="conserved hypothetical
 protein"
 /protein-id="AAM83939.1"
 /db-xref="GI:21957033"
 /translation="MGSRDDNNGSLNLPSIVDLS
 TNANFQPDGTL LASATSDFTTFAV
 NTGYALDQVLFRCDAADV DQLYEMYATNGDSTYG
 GRYEDGTIAGNVSYGYATTVMNVV
 IRFTNLATGEYYARIWKGRRLTGLDTDSSGRILV
 KAKNFSNVYTELFRIDYARSGANN
 TPSYLYGRSQPNAYIAFKGPGITGPIEGTDSYSN
 WPGWYSTWPASLGLYKYVTFRRTT
 ICAVSNFTPTTVLPRISVAELNNGNTSSADFNVD
 FQCQTGINSQV TAGTVAMGFLVPA
 ANAAKAQALGLMNGNGGVSHLVSDNYGAAGTAGG
 VGIRIYRNNSPMYLLSKNVTQTGN
 NGGWYGILQGAQETTGSVDGGNSYTETFRAELSK
 ISGQTVTAGAVNAHAQVVIRVQ"
 gene complement(389158..3917 /gene="fimD"
 85)
 /locus-tag="y0350"
 CDS complement(389158..3917 /gene="fimD"
 85)
 /locus-tag="y0350"
 /function="membrane; cell
 envelope: outer membrane
 constituents"
 /note="fimbrial biogenesis;
 residues 31 to 874 of 875 are
 46.38 pct identical to residues 25
 to 860 of 872 from GenPept :
 >gb|AAG05518.1|AE004640-7
 (AE004640) probable fimbrial
 biogenesis usher protein
 [Pseudomonas aeruginosa]"
 /codon-start=1
 /transl-table=11
 /product="outer membrane usher
 protein FIMD precursor"
 /protein-id="AAM83940.1"
 /db-xref="GI:21957034"
 /translation="MVQARVILKKNFSGRRKALT
 LCITLILHIDTAFGQEEPQNFEFD
 ESLFLGTKYASGLTQLNKKNSITAGNYDAVDVLV
 NNKLFKRMSVQFIKDANSSEVYPC
 LSDELLTAAGVELGRENSTPPKEPHVTEANTPIT
 ETHAPTNQCLPLSTRVKGASFRFD
 QAKLRLELSIPQALLQKRPRGYIERAEWQEGEKL

AFINYSANAYRSDTRGQQKRTSDF
 GFIGLKSGINLGLWQVRQQSNVRYASNDSGSDTQ
 WNSIRTYVQRP IPQLDSQLTLGET
 FTDSTLFGSMSFLGAKMATDQRMWPVSMRGFSPE
 VRGVASTNARV IIRQNGREIYETN
 VAPGPFVINDLFSTSSQGDLNVEVIEANGSRSTF
 TVPFSAPVDSMRPGVSRYNAVIGE
 SRDFTNIDNYFTDFTYERGLTNQLTANSGVRLAK
 DYTALLAGGVLGTPVGALGLNATY
 SHAKVENDKTQDGWRMQATYSQTFNQGTGTTFSLA
 GYRYSTKGYRDLNDVFGVRSMQKN
 GGTWDSSTYKQRSQFTTTINQDLGNWGQLYASAS
 TSDYYNDTARDTQLQLGYSNSYQQ
 ISYNLAVSRQRSVYTSTLYNWDSPDTDETATTTT
 YGNTENIATFTVSIPLNIGSNNQY
 LSMSASRNPKSGNNYQTSLSGTAGERNSFNALN
 AGYDDSNFGSSSNNWGANVQKQFP
 NATVNGSYSRGNNYTQYGAGARGAAVIHRQGVTL
 GPYLGETFGLIEANGAQGARIDSN
 GFALVPALTPYNYNTIGLDTKGINRNTELKENQG
 RVVPYAGAAVKVKFETLTGYAVLI
 QAEGEGLPLGADVNSKDELVGMVGGNQIYARI
 ADNKGTL DVRWGESSGDQCQLPYA
 FNRQDTEQDIIHITASCRR"

gene complement (391813..3925 /locus-tag="y0351"
 68)
 CDS complement (391813..3925 /locus-tag="y0351"
 68)

/function="putative factor;
 folding and ushering proteins:
 Chaperones"
 /note="pilus assembly; residues 24
 to 242 of 251 are 43.69 pct
 identical to residues 16 to 237 of
 248 from GenPept :
 >gb|AAG05517.1|AE004640-6
 (AE004640) probable pili assembly
 chaperone [Pseudomonas
 aeruginosa]"
 /codon-start=1
 /transl-table=11
 /product="chaperone"
 /protein-id="AAM83941.1"
 /db-xref="GI:21957035"
 /translation="MTSEGLIMLSIYARHYHYL
 FVTLLVAMSLSFANASVVMTGSR I
 IYPAAASEHSIQLTNNDNFPNAVQVWLD SGDEKS
 TPETGKAPFIVTPPFFRIEANSQ
 TLRKLTGSGLPTDRESVFYLNFLQIPPVNKVEK
 DNKMLVLLRNRIKVFYRPESIIGR
 VDQVSTALTFSLRKQGTNLVLTGKNPTGFYATIA
 SGEIVSGSIKLKVKSNMIAPMSQV
 EWVIPNASVSSSATINFLIMNDFGGQDAGSYRI"

gene complement (392608..3931 /locus-tag="y0352"
 38)
 CDS complement (392608..3931 /locus-tag="y0352"
 38)

/function="structural component;
 cell exterior constituents:
 surface structures"
 /note="fimbrial biogenesis;
 residues 1 to 175 of 176 are 49.15


```

pct identical to residues 3 to 177
of 178 from GenPept :
>gb|AAL19294.1| (AE008710)
putative fimbriae; major subunit
[Salmonella typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="fimbrial protein
(precursor)"
/protein-id="AAM83942.1"
/db-xref="GI:21957036"
/translation="MKKITLAIALFSASTTVAMS
ASNNTITFQGEVTAQTCSVTVNGL
EANPVVLLPTVSSSDLASGQTKGKTTFTLGVSG
CTSGSDDLDIKTVFIGSLVTATGN
LQNTGTAGNVELQLLKDATTTTGIDLNSGLAQDG
IVLLAGDTSAEHDFAVQYYATGQS
TPGSVIASVQYAVSYL"
repeat-region complement(393913..3952 /note="insertion element"
27)
gene complement(393948..3951 /insertion-seq="IS285"
56) /locus-tag="y0353"
CDS complement(393948..3951 /locus-tag="y0353"
56)
/function="IS and transposon
related functions"
/note="residues 1 to 402 of 402
are 100.00 pct identical to
residues 1 to 402 of 402 from
GenPept : >gb|AAC13227.1|
(AF053947) transposase [Yersinia
pestis]"
/codon-start=1
/transl-table=11
/product="putative transposase"
/protein-id="AAM83943.1"
/db-xref="GI:21957038"
/translation="MDEKKLKALAAELAKGLKTE
ADLNAFSRMLTKLTVETALNAELT
EHLGHEKNTPKSGSNTRNGYSSKTLCCDDGEIEL
NTPRDRENTFEPQLIKKNQTRITQ
MDSQILSLYAKGMTTREIVATFKEMYDADVSPTL
ISKVTDVKEQVAEWQNRQLDALY
PIVYMDCIVVKVRQNGSVINKAVFLALGINTEGQ
KELGLMWLAENEGAKFWLSVLTEL
KNRGLQDILIAVDGLKGFPDAINSVYPQTHIQL
CIIHMRNSLKYVSWKDYKAVTSG
LKMVYQAPTEEAALMALDKFAEAWDDKYPQISKS
WRTHWENLNTFFGYPPDIRKAIYT
TNAIESVNSVIRAAIKKRKFPTDDSVRKVVYLA
IKDASKKWSMPIQNWRLAMSRFII
EFGDRLSDHL"
gene complement(395253..3960 /locus-tag="y0354"
44)
CDS complement(395253..3960 /locus-tag="y0354"
44)
/function="enzyme; global
regulatory functions"
/note="residues 8 to 258 of 263
are 39.45 pct identical to
residues 3 to 256 of 288 from

```

		GenPept : >gb AAC27745.1 (AF061240) glutamine cyclotransferase precursor [Carica papaya]" /codon-start=1 /transl-table=11 /product="glutamine cyclotransferase" /protein-id="AAM83944.1" /db-xref="GI:21957039" /translation="MEILNIPRRCFTFLIIITY SFPLSFADSKPLKYTFEVIRKIPH DETSFTQGLVIDDGKLYETTGLYKNSKIRELDLT NGKVIRSVNLPDNIFGEGITKLGD SFYVLTWKEKKAFVINPNDLKIIKTFNYEGEGWG LTTDGINLIMDGSDTLYFRNPAD FSIKKISVTFDGRRIEKINELEWIDGMIYANVW YSDAILVIEPENGRRVVKWIELSGL QFMLDSVNRNTNTLNGIAYDKSKNKIYLTGKNWS NIFEVKFLTSK"
gene	complement(396283..396579)	/gene="ppiC" /locus-tag="y0355"
CDS	complement(396283..396579)	/gene="ppiC" /locus-tag="y0355" /function="enzyme; proteins - translation and modification" /note="rotamase C; residues 6 to 98 of 98 are 67.74 pct identical to residues 1 to 93 of 93 from E. coli K12 : B3775" /codon-start=1 /transl-table=11 /product="peptidyl-prolyl cis-trans isomerase C" /protein-id="AAM83945.1" /db-xref="GI:21957040" /translation="MVTVTMANKASALHILVDDE KQANDILAQLNNGANFQELAKKFS NCPSKRNGDLGEFNKGDMPAFDKAVFSCCELLQ PYGPVKTQFGYHIIKVLIRS"
gene	396714..398789	/gene="rep" /locus-tag="y0356"
CDS	396714..398789	/gene="rep" /locus-tag="y0356" /function="enzyme; DNA - replication, repair, restriction/modification" /note="residues 19 to 686 of 691 are 85.02 pct identical to residues 1 to 668 of 673 from E. coli K12 : B3778; residues 19 to 686 of 691 are 85.32 pct identical to residues 1 to 668 of 673 from GenPept : >gb AAG58972.1 AE005609-4 (AE005609) rep helicase, a single-stranded DNA dependent ATPase [Escherichia coli O157:H7 EDL933]" /codon-start=1

		coli K12 : B3780"
		/codon-start=1
		/transl-table=11
		/product="putative ATP-dependent
		RNA helicase"
		/protein-id="AAM83948.1"
		/db-xref="GI:21957043"
		/translation="MSKTHLTEQKFSDFALHPLV
		VEALENKGFQYCTPIQALALPLTL
		SGRDVAGQAQTGTGKTLAFLASTFHYLLSHPAEE
		GRQTNQPRALIMAPTRELAVQIHS
		DAESLSQVTGLKLGLAYGGDGYDKQLKVLESGVD
		ILIGTTGRLIDYAKQNYINLGAIQ
		VVVLDEADRMVDLGFIKDIRWLFRRMPSVDKRLN
		MLFSATLSYRVRELAFEQMNNAEY
		VEVEPLQKTGHRIKEELFYPSNEEKMRLLQTLIE
		EEWPDRCIIFANTKHRCEEIWGHL
		AADGHRVGLLTGDVAQKKRLRILEDFTKGDLIDIL
		VATDVAARGLHIPLVTHVFNVDLP
		DDCEDYVHRIGRTGRAGESGHSISLACEEYALNL
		PAIETYTGHSIPVSKYNSDALLTD
		LPAPKRLARTRTGNGPRNSAPRRSGAPRNNRKR
		PG"
gene	401861..402187	/gene="trxA"
		/locus-tag="y0360"
CDS	401861..402187	/gene="trxA"
		/locus-tag="y0360"
		/function="enzyme; biosynthesis of
		cofactors, carriers: Thioredoxin,
		glutaredoxin, glutathione"
		/note="residues 1 to 108 of 108
		are 87.03 pct identical to
		residues 19 to 126 of 127 from E.
		coli K12 : B3781; residues 1 to
		108 of 108 are 87.03 pct identical
		to residues 1 to 108 of 109 from
		GenPept : >gb AAC40210.1
		(AF044308) Escherichia coli
		thioredoxin [Cloning vector
		pBIOTRX-BirA]"
		/codon-start=1
		/transl-table=11
		/product="thioredoxin 1"
		/protein-id="AAM83949.1"
		/db-xref="GI:21957044"
		/translation="MSDKIIHLSDDSFDTDLKA
		SGLVLVDFWAEWCGPCKMIAPILD
		EIAEEYEGRLTIAKLNIDDNQGTAPKYGIRGIPT
		LLLFRDGEVVATKVGALSKGQLKA FLDANL"
gene	402667..403926	/gene="rho"
		/locus-tag="y0361"
CDS	402667..403926	/gene="rho"
		/locus-tag="y0361"
		/function="factor; RNA synthesis,
		modification, DNA transcription"
		/note="residues 1 to 419 of 419
		are 95.22 pct identical to
		residues 1 to 419 of 419 from E.
		coli K12 : B3783"
		/codon-start=1
		/transl-table=11
		/product="transcription

		termination factor Rho; polarity suppressor" /protein-id="AAM83950.1" /db-xref="GI:21957045" /translation="MNLTELKNTPTVSDLITLGEN MGLENLARMRKQDIIFSILKQHAK SGEDIFGDGVLEILQDGFGLRSADSSYLAGPDD IYVSPSQIRRFNLRTGDTVAGKIR PPKEGERYFALLKVNEVNYDKPENARNKILFENL TPLHANSRLRMERGNSTEDLTAR VLDLASPIGRGQRGLIVAPPKAGKTMMLQNIATS IAYNHPDCVLMVLLIDERPEEVTE MQRLVKGEVIASTFDEPASRHHVQVAEMVIEKAKR LVEHKKDVIILLDSITRLARAYNT VVPASGKVLTTGGVDANALHRPKRFFGAARNVEEG GSLTIIATALVDTGSKMDEVIYEE FKGTGNMELHLSRKIAEKRVFPAIDFNRSCTRKE ELLTTTDELQKMWILRRILHPMGE IDAMEFLISKLATAKTNDQFFDNMRRS" /gene="rfe" /locus-tag="y0362" /gene="rfe" /locus-tag="y0362" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="synthesis of enterobacterial common antigen (ECA); residues 1 to 357 of 365 are 80.95 pct identical to residues 1 to 357 of 367 from E. coli K12 : B3784; residues 1 to 357 of 365 are 81.23 pct identical to residues 1 to 357 of 367 from GenPept : >gb AAG58979.1 AE005610-3 (AE005610) UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase; synthesis of enterobacterial common antigen (ECA) [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="UDP-GlcNAc:undecaprenylp hosphate GlcNAc-1-phosphate transferase" /protein-id="AAM83951.1" /db-xref="GI:21957047" /translation="MNLLTMSTELIYIFLFSMAF LFVARKVAIKIGLVDPNYRKRHQ GLIPLVGGISVFAGVCFAFLITNQQIPHFRLYLA CAGLLVVFVGGALDDRFDISVKIRAF VQALVGIAMMAVAGLYLRSLGHAFGPWEMVLGPF GYVVTLFVWAAINAFNMVDGIDG LLGGLSCVSFGAMGILLYQSGQMSLALWCFAMIA TIIPYILLNLGLLGRRYKVFMDA GSTLIGFTAIWILLQATQGNAHPINPVTALWIIA IPLMDMIAIMYRRLRKGMSPFSPD RQHIHHLIMRAGFTSRQAFVLITLAAALLAMIGV IGERLTFIPEWVMLALFLLAFLLY
gene	404461..405558	
CDS	404461..405558	

gene	405576..406655	GYCIKRAWRVARFIKRFKRRMRASKNKHES"
		/gene="wzzE"
		/locus-tag="y0363"
CDS	405576..406655	/gene="wzzE"
		/locus-tag="y0363"
		/function="putative transport"
		/note="residues 22 to 357 of 359
		are 68.15 pct identical to
		residues 15 to 349 of 349 from E.
		coli K12 : B3785"
		/codon-start=1
		/transl-table=11
		/product="putative transport
		protein"
		/protein-id="AAM83952.1"
		/db-xref="GI:21957048"
		/translation="MMKPESMSTDKTGSTNNEPS
		VDNELDIRGLCRTLWRGKVWIIGM
		AIIFAAIALGVSYLVKQWSATAITDKPTVNNLG
		GYYSQQQFLRNLDIRLNSGLVSEQ
		PGISDEAYGEFITQLAAYDTRDFWLQSDYYKQR
		LEGDAKADAALLDELVNNIVFTAR
		DDKKIPNDSIKLTAETASDANKLLRGYIDFASQR
		ASSHLNDEIQGAWAARTQSMKAQV
		KRQEAVAQAVFDREVAAVKQALKVAGQQGITSSQ
		TDTPAEQLADSKMFMLGKPMLEAR
		LETLLATGPSFDDIDYDQNRAMLATLNVGPTLDDK
		FQTYRYLRTPEDPVTRDSPRRVFL
		LIMWGAIGALVGAGVVLVRRSSKAL"
gene	406882..408066	/gene="wecB"
		/locus-tag="y0364"
CDS	406882..408066	/gene="wecB"
		/locus-tag="y0364"
		/function="enzyme; central
		intermediary metabolism:
		Sugar-nucleotide biosynthesis,
		conversions"
		/note="synthesis of
		enterobacterial common antigen
		(ECA); residues 15 to 394 of 394
		are 78.15 pct identical to
		residues 11 to 389 of 389 from E.
		coli K12 : B3786; residues 15 to
		394 of 394 are 78.42 pct identical
		to residues 11 to 390 of 390 from
		GenPept :
		>gb AAG58981.1 AE005610-5
		(AE005610) UDP-N-acetyl
		glucosamine -2-epimerase;
		synthesis of enterobacterial
		common antigen (ECA) [Escherichia
		coli O157:H7 EDL933]"
		/codon-start=1
		/transl-table=11
		/product="UDP-N-acetyl glucosamine
		-2-epimerase"
		/protein-id="AAM83953.1"
		/db-xref="GI:21957049"
		/translation="MRPTCRHCLRLTDLKRFTVK
		VLTVFGTRPEAIKMAPLVHALAQD
		DAFESRVCVTAQHREMLDQVLRLEIQQPDYDLDI
		MRPGQGLTEITCRILEGLKPVLEE

gene	408063..409325	FKPDVILVHGDTTTTLSASLAGFYHRIPVGHVEA GLRTGDLYSPWPPEANRQLTGHLA MYHFAPTENSRQNLLREWVPENRIFVTGNTVIDA LFWVRDRVMNTPDLRANLAQRYAF LDTNKKMILVTGHRRESFGGGFERICSALAEIAR KHPEVQVVYPVHLNPNVSEPVNRI LKGIDNIILIDPQDYLFPVYLMNHAYLILTDSGG IQEEAPSLGKPVLMRDTERPEA VDSGTVLLVGTNINKIVDAVTRLLTDETAYHQMT RAHNPPYGDGYACQRILKALKNHQV TL"
CDS	408063..409325	/gene="wecC" /locus-tag="y0365" /gene="wecC" /locus-tag="y0365" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="synthesis of enterobacterial common antigen (ECA); residues 1 to 420 of 420 are 82.14 pct identical to residues 1 to 420 of 420 from E. coli K12 : B3787; residues 1 to 420 of 420 are 83.57 pct identical to residues 1 to 420 of 420 from GenPept : >emb CAD09395.1 (AL627279) UDP-ManNAc dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="UDP-N-acetyl-D-mannosami nuronic acid dehydrogenase" /protein-id="AAM83954.1" /db-xref="GI:21957050" /translation="MSFETISVIGLGYIGLPTAA AFASRKKKVIGVDVNAHAVETINR GAIHIVEPDLDKVVKIAVEGGYLQAVTKPQAADA FLIAVPTPFKGDHEPDMIFVESAA KSIAPVLKKGDLVILESTSPVGATEQMAQWLAE RPDLSFPQQAGEAADINIAYC PER VLPQGVMEVLIQNDRVIGGMPKCSARASALYKI FLEGECVVTNSRTAEMCKLTENSF RDVNIAFANELSLICDEQGINVWELIRLANRHP RVNILQPGPGVGGHCIAVDPWFIVS QNPQLARLIHTARLVNDGKPLWVVDVKA AAVADC LAASDKRASEVKIACFGLA FKPDI DDLRESPAVGVARLIAEWHVGETLVVEPNVEQLP KSLMGLVTLKDTATALQQADVLVM LVDHKQFKAIKPEDIKQQWIVDTKGVWR"
gene	409316..410389	/gene="rffG"
CDS	409316..410389	/locus-tag="y0366" /gene="rffG" /locus-tag="y0366" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="residues 3 to 355 of 357 are 82.15 pct identical to residues 1 to 353 of 355 from E.

		coli K12 : B3788; residues 1 to 357 of 357 are 85.43 pct identical to residues 1 to 357 of 357 from GenPept : >gb AAC12869.1 (AF044332) dTDP-D-glucose-4,6-dehydratase; RffG [Pectobacterium carotovorum subsp. atrosepticum]" /codon-start=1 /transl-table=11 /product="dTDP-glucose 4,6-dehydratase" /protein-id="AAM83955.1" /db-xref="GI:21957051" /translation="MALRRILVTGGAGFIGSAVV RHIIDGTSDSVVVVDKLTAGNLE SLSVVAGSERYAFEQVDICDSSELDVFAQYQPN VVMHLAAESHVDRSIDGPAAFIET NVVGTYTLLEAARHYWQQLSVEAKQAFRFHHIST DEVYGDHLHGTDLFTETTPYAPSS PYSASKASSDHLVRAWLRTYGLPTLVNCSNNY PYHFPEKLIPLVILNALAGKPLPV YGNGAQVRDWLYVEDHARALYQVVTGVVGETYN IGGHNERKNIEVVETICALLDLV PAKPAGIAHYRDLITYVKDRPGHDMRYAIDAGKI ERELGWRPQETFESGIRKTVLWYL NNESSWRRVQDGSYAGERLGLSD" /gene="rffH" /locus-tag="y0367"
gene	410474..411565	
CDS	410474..411565	/gene="rffH" /locus-tag="y0367" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="residues 71 to 363 of 363 are 86.68 pct identical to residues 1 to 293 of 293 from E. coli K12 : B3789" /codon-start=1 /transl-table=11 /product="glucose-1-phosphate thymidyltransferase" /protein-id="AAM83956.1" /db-xref="GI:21957052" /translation="MLAAFLHLEIYSVYRWATYE RHQSRLIIGMASSRLHDVLPVYS LCLMVSGDGMVQEIVCIRRLHVSGERMKGIILAG GSGSRLHPITRGVSKQLLPIDKP MIYYPLSVLMLAGIRDVLIISTPEDLPSFQRLLG NGDEFGINLSYAAQSPDGLAQAF IIGAFIDNEPCCLVLGDNIYFGQGFSPKLKAVA ARQQGATVFGYQVMDPERFGVVEF DDNFRALSIEEKPSQPKSNWAVTGLYFYDNQVVD FAKQVKPSARGELEITSINQMYLD RGELTVELLGRGFAWLDTGTHDSLIEASTFVQTV EKRQGFKIIACLEEIARNGWLDDD GVKRAATALAKTGYGKYLLDLLHARPRQY" /gene="wecD" /locus-tag="y0368"
gene	411486..412280	
CDS	411486..412280	/gene="wecD" /locus-tag="y0368"

		/note="residues 63 to 263 of 264 are 49.25 pct identical to residues 1 to 181 of 181 from E. coli K12 : B3790" /codon-start=1 /transl-table=11 /product="hypothetical protein" /protein-id="AAM83957.1" /db-xref="GI:21957053" /translation="MRQPRWRKPVMANICWIIYM PVHASIEPLGWESEFFQRQSAKLI FSDSAPPLNPAELAAFTLVQAKVPTHRLDLIDAL SQLDFHLVEGEIDLSLVVGEKEGI GTENATSEPNMGAYSLRVATEADIPQLRRVAASA FALSFRAPWYDAQDSGRFYALWV EKAVLGTDFDHQCLLVLDPTDQPVGFVTLRDLQDG SARIGLLAVFPGAQSKGIGLRRLMS AAKQWCQHHGLHRLRVATQMSNIAALRLYIRSGA SIESTAYWLCRG"
gene	412207..413412	/gene="wecE"
CDS	412207..413412	/locus-tag="y0369" /gene="wecE" /locus-tag="y0369" /function="putative regulator" /note="residues 26 to 400 of 401 are 84.79 pct identical to residues 1 to 375 of 376 from E. coli K12 : B3791" /codon-start=1 /transl-table=11 /product="putative regulator" /protein-id="AAM83958.1" /db-xref="GI:21957054" /translation="MLLYVSIFVVVPLRVPRIG YAGDEMIPFNTPIVGTGELGYMQA AMSSGKLCGDDGGFTRRCQQWMEKRFNCPKVLTP SCTASLEMAALLLDIKPGDEVIMP SFTFVSTANAFVLRGAKMVFDIRPDTMNIDETK IEAAITDKTRVIVPVHYAGVACEM DTIMALAKKHNLFFVEDAAQGVMSYKKGALGTI GHIGCFSFHETKNYTAGGEGGATL INDPSLIDRAEIIREKGTNRSQFFRGQVDKYTW DIGSSYLMSDLQAAYLWGQLEAAE QINERRLALWHGYNAFKPLADAGRIDLVPVPGN VVQNAHMFYIKLRDIEERSAFISY LKEADIMAVFHYIPLHACPAGEAFGRMAGEDRFT SKESERLVRLPIFYNLTDVNQSTV INTVLSFFV"
gene	413414..414670	/gene="wzxE"
CDS	413414..414670	/locus-tag="y0370" /gene="wzxE" /locus-tag="y0370" /function="putative carrier" /note="residues 1 to 416 of 418 are 75.00 pct identical to residues 1 to 416 of 416 from E. coli K12 : B3792; residues 1 to 416 of 418 are 75.00 pct identical to residues 1 to 416 of 416 from GenPept : >emb CAD09390.1 (AL627279) putative lipopolysaccharide biosynthesis

		protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="putative cytochrome" /protein-id="AAM83959.1" /db-xref="GI:21957055" /translation="MSLAKASIWTACSTLIKIGV GLLVVKLLAVTFGPSGVGQAGNFR QLIIVLGVLSGAGIFNGITKYVAEYHQQPERLRA MLGTSSTIVLGFSTLLALVFLLAA KPVSIALFGHADYQNVVRAIAFIQMGIAYGNLFL AILKGYRDAMGNALAIIGGSLIGV VAYYICFQIGGYSGALVGLGLVPALVVLPAAML YRRRTIPLRYLKPHWDKALASHLG KFTLMALITSVTLPVAYVMMRHLLANNYGWDAVG IWQGVSSISDAYLQFITASFTVYL LPTLSRLKDKGAISREIFRSLKFVLPAAVAASLT VWLLRDFAIWLLFSHQFTAMRDLF AWQLVGDVCLKVGSYVFGYLVIAKASLRFYILA EQVLLLTGFAYWLIPMNGSLGAAQ AYMATYIVYFALCSCAFLVYRRHSAP"
gene	414693..415778	/gene="wecF"
CDS	414693..415778	/locus-tag="y0371" /gene="wecF" /locus-tag="y0371" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="synthesis of enterobacterial common antigen (ECA); similar to B3793 in E. coli K-12; residues 1 to 359 of 361 are 64.90 pct identical to residues 1 to 357 of 359 from GenPept : >emb CAD09389.1 (AL627279) conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi]" /codon-start=1 /transl-table=11 /product="TDP-Fuc4NAc:lipid II Fuc4NAc transferase" /protein-id="AAM83960.1" /db-xref="GI:21957056" /translation="MITLTHVLGSDIPHHNLTVL RFFNDVLAKCLPVEQVRHFMVAAK ETAPFSSFPQLDINTYSDKKALAEAVIARAQADR SARFFWHGQFNVTLLWLALLSGKIK PGQVYWHVWGADLYEDAKSLKFRLFYLLRRIAQG RVGHVFATRGLIHYYQQRHPRVPA SLLYFPTRMDPALTAIDKPLAGPMTILVGNSG DTTNRHIEALKAIHQFGPDVRVI IPMGYPANNEAYIEQVRQAGLALFSQDNLRLITE QIPFDDYLNILRECDLGYFIFNRQ QGIGTLCLLTQFGVPFVLSRKNPFWQDLAEQH IPVFFYGDTLDEPMIREAQRLAGLD KQAIAFFNPNIIEGWKQALALAAAGEHP"
gene	415775..417139	/gene="wecF"
CDS	415775..417139	/locus-tag="y0372" /gene="wecF"

		/locus-tag="y0372" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="synthesis of enterobacterial common antigen (ECA); residues 1 to 444 of 454 are 77.97 pct identical to residues 1 to 445 of 450 from E. coli K12 : B3793; residues 1 to 444 of 454 are 77.97 pct identical to residues 1 to 445 of 450 from GenPept : >gb AAG58989.1 AE005610-13 (AE005610) TDP-Fuc4NAc:lipidII transferase; synthesis of enterobacterial common antigen (ECA) [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="TDP-Fuc4NAc:lipidII transferase" /protein-id="AAM83961.1" /db-xref="GI:21957057" /translation="MTLGQFGGLFCIYLIIVIFI LTLTYQEFRRVKFNFNVLFSMLYL LTFYFGFPLTCMLVFQFGVAVVPVEYLLYAMLSA TAFYGIYVITYKTRLRQPRSQPRT PIFTMNRVETNLTWVLLALVAVGTVGIFFMQNGF LLFKLDSYSKIFSSDVSGVALKRF FYFFIPAMLVVYFLKQDRRAWFFFLASTVAFGIL TYVIVGGTRANIIIAFSLFLFIGI VRGWITLWMLAAAGVFGIVGMFWLALKRYGLDVN GAFAFYTFLYLTRDTFSPWENLGL LLQNYDKIDFQGLAPIVRDFYVFIPSALWPERPD LVLNTANYFTWDVLDNHSGLAISP TLIGSLVVMGGVLFIPLGAIVVGLIIKWFDWLYE QGKAESNRYKAAILQSFCFGAVFN IIVLAREGLDSFVSRVFFCVIFGACLVLAKLLY WLFDTAGLIKRGQIKSNRLSTPNA GNQL" /gene="wecG" /locus-tag="y0373" /gene="wecG" /locus-tag="y0373" /function="enzyme; central intermediary metabolism: Sugar-nucleotide biosynthesis, conversions" /note="synthesis of enterobacterial common antigen (ECA); residues 1 to 246 of 246 are 70.73 pct identical to residues 1 to 246 of 246 from E. coli K12 : B3794" /codon-start=1 /transl-table=11 /product="probable UDP-N-acetyl-D-mannosaminuronic acid transferase" /protein-id="AAM83962.1"
gene	417148..417888	
CDS	417148..417888	

		/db-xref="GI:21957058" /translation="MEPNTVIPKYNVRGFEIWGF RDMAQVLDHLLGSGPVKTGTLVAM NAEKLLKAEDDTALCELIKNAEYLYADGISMVRA IRRKYPQAELSRVAGADLWEALMQ RAGQQGTPVFLVGGKPDVLAETEAQLRAQWNVNL VGSQDGYFTPEQREALFARIAASG AAIVTVAMGSPKQEIFMRDCRKFYPDALYMGVGG TYDVFTSHVKRAPKIWQNMGLEWL YRLLAQPSRIRRQLKLLKFVGYYYSGRL"
gene	complement(418178..418261)	/locus-tag="y0374"
CDS	complement(418178..418261)	/locus-tag="y0374"
		/codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM83963.1" /db-xref="GI:21957060" /translation="MNEGLTAPRGTPVAYATTP TARFPFN"
gene	418412..419803	/locus-tag="y0375"
CDS	418412..419803	/locus-tag="y0375" /function="putative transport" /note="residues 1 to 454 of 463 are 79.73 pct identical to residues 1 to 452 of 461 from E. coli K12 : B3795; residues 1 to 454 of 463 are 80.39 pct identical to residues 1 to 452 of 461 from GenPept : >gb AAG58991.1 AE005611-1 (AE005611) putative amino acid/amine transport protein [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="putative amino acid/amine symporter" /protein-id="AAM83964.1" /db-xref="GI:21957061" /translation="MADNAEKKGLHRGLEARHIE LIALGGTIGVGLFMGSASTLKWAG PSVLLAYIIAGLFVFFIMRAMGEMLYLEPVAGSF AVYAHKYLSPYFGYLTAWGYWFMW IAVGISEITAIGVYVQFWFPEIPQWLPAIAGVAI VALANLAAVKLYGELEFWFAMIKV TTIIVMILVGLGVIFFGFGNHGQPIGFDNLTAHG GFFAGGWKGFLFALCIVVASYQGV ELVGITAGEARNPQVTLRRAINNILWRILIFYVG AIFVIVTIFPWNIGIGTEGSPFVLT FAKIGIVAAAGIINFVILTAALSGCNSGMYSGR MLYALAKNRQLPAGLTKLSASGVP VYCIAITILCLLVGSSSLNYIIPNPQQVFVYVYSA SVLPGMVPWFVVLVCQLRFRQVHK AALQQHPFKSILFPYVNYLTIAFLICVLVGMGIN PDTRLSELLVGAIFLALVTGCYFVL GMHKPKAMEAERL"
gene	419952..420025	/locus-tag="yt006"
tRNA	419952..420025	/locus-tag="yt006" /product="tRNA-Arg" /note="anticodon: CCG"

gene	420112..420184	/locus-tag="yt007"
tRNA	420112..420184	/locus-tag="yt007"
		/product="tRNA-His"
		/note="anticodon: GTG"
gene	420204..420287	/locus-tag="yt008"
tRNA	420204..420287	/locus-tag="yt008"
		/product="tRNA-Leu"
		/note="anticodon: CAG"
gene	complement(420253..420741)	/locus-tag="y0376"
CDS	complement(420253..420741)	/locus-tag="y0376"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM83965.1"
		/db-xref="GI:21957062"
		/translation="MIFNIFNELNVTFSRQCDRL LLSWKTNTDAQHNETAQLTVLAAE CDQRELIMEVINKVPVARRIRRIKGGKLQVGLSV WQNRIIIFRRKKTTPHCGVSSEIGR RERIRTS DPLVPNQLRYQAALLADFLLLTLHGSL TYVHV NINKYLHVCVVRREGLEPS RP"
gene	420366..420439	/locus-tag="yt009"
tRNA	420366..420439	/locus-tag="yt009"
		/product="tRNA-Pro"
		/note="anticodon: TGG"
repeat-region	421164..421873	/note="insertion element"
		/insertion-seq="IS1541a"
gene	421258..421767	/locus-tag="y0377"
CDS	421258..421767	/locus-tag="y0377"
		/function="IS and transposon related functions"
		/note="IS1541a; residues 1 to 169 of 169 are 100.00 pct identical to residues 1 to 169 of 169 from GenPept : >gb AAC82673.1 (AF074611) transposase [Yersinia pestis]"
		/codon-start=1
		/transl-table=11
		/product="putative transposase"
		/protein-id="AAM83966.1"
		/db-xref="GI:21957063"
		/translation="MRSGNCKCSTRNQKGVPMRD EKSLAHTRWNCKYHIVFAPKYRRQ VFYREKRRRAIGSILRKLC EWKNVNILEAEYCVDH IHMLLEIPP KMSVSGFMGYLKGKS SLMLYEQFGDLKFKYRNREFWCRGYVDTVGKNT ARIQEYIKHQLEEDKMGEQLSIPY PGSPFTGRK"
gene	complement(421960..423180)	/gene="hemY"
		/locus-tag="y0378"
CDS	complement(421960..423180)	/gene="hemY"
		/locus-tag="y0378"
		/function="enzyme; biosynthesis of cofactors, carriers: Heme, porphyrin"
		/note="a late step of protoheme IX synthesis; residues 1 to 395 of

```

406 are 70.63 pct identical to
residues 1 to 395 of 398 from E.
coli K12 : B3802"
/codon-start=1
/transl-table=11
/product="hemY protein"
/protein-id="AAM83967.1"
/db-xref="GI:21957064"
/translation="MLRVLLLFLVLTIVGIVLGPM
LAGHQGYVLIQTDNYNVTTSTVGL
AIMLVLLLVAFFIVEWVLRRIFRGTARGWFLG
RKRTARNQMKAALIKLAEGDFLQ
VEKLLTRNADHAEQPMVNYLLAAEAAQQRGDEF
TNQYLERAAEVADGDQLPVNITRV
RIQLAQGHIHAARHGVDRLLDQAPRHPEVLR
LAEQAYLRSGAYRSLLDILPAMSKTQI
HTPEEVAALEQQAYIGIMNQCMADGSEGLKR
WWDKQSRKVRNEIPLQVALAEHLIEC
DDHDVAQKIILDSLKHQYDERLALLIPRLK
AGNPEPLEKSLRQQIKQHGGATPLLNSTL
GQLMLKHGEWEKASEAFKAALQRPDGYDYA
WLA DALDKLHRPEDAAQARREGLLLTL
RQNGESSALTKLIH"
gene      complement(423183..4243 /gene="hemX"
16)
CDS      complement(423183..4243 /gene="hemX"
16)
/locus-tag="y0379"
/function="enzyme; biosynthesis of
cofactors, carriers: Heme,
porphyrin"
<-----User Break----->
145 of 145 are 46.15 pct identical
to residues 1 to 126 of 127 from
GenPept : >gb|AAL22425.1|
(AE008864) putative
acetyltransferase [Salmonella
typhimurium LT2]"
/codon-start=1
/transl-table=11
/product="hypothetical protein"
/protein-id="AAM84010.1"
/db-xref="GI:21957111"
/translation="MNLGAISTLLLWLLAMKLT
IERLITLTHQDVIDLAKIWPNQQA
AWQQWITEGRPLFAARFNERLLGAVKVAVYD
QQA ELQDLCVREVTRRRGVGLYLIEET
LRQLPEIKHWYLNGGDLTAAERPQMNSFML
ACGFSHEAQGWRR"
gene      470375..471505 /gene="livK"
CDS      470375..471505 /gene="livK"
/locus-tag="y0422"
/function="transport; transport of
small molecules; amino acids,
amines"
/notes="residues 12 to 376 of 376
are 75.34 pct identical to
residues 6 to 369 of 369 from E.
coli K12 : B3458; residues 12 to
376 of 376 are 75.61 pct identical

```

		to residues 6 to 369 of 369 from GenPept : >gb AAG58565.1 AE005569-5 (AE005569) high-affinity leucine-specific transport system; periplasmic binding protein [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="high-affinity leucine-specific leucine-specific-b inding periplasmic protein of high-affinity branched-chain amino acid ABC transporter transport system; periplasmic binding protein" /protein-id="AAM84011.1" /db-xref="GI:21957112" /translation="MGNSRMKLTGKGVLLAGCMA MAMSHSVLAQDIKVAIVGAMSGPV AQYGDMQFTGARQAIADINASGGIKGDKLVGVEY DDACDPKQAVAVANKVINDGIRYV IGHLCSSSTQPASDIYEDEGVIMITPAATNADLT TRGYKMIMRTTGLSDQGPTAAKY IVETIKPKRIAVVHDKQQYGEGLARSVRDSLKEQ GAEVVLFEGVTAGDKDFSTLVARL KKENVDFVYFGGYYPEMGQILRQAKQAGLTARFM GPEGVGNSSLSNIAGEASEGMLVT LPKRYDQVPANQPIVDALKAKKLDPTGPFVWTTY AALQSLTTAMERTGSKEPADLAND LKTGKPVETVMGPLSWDDKGD LKGF EFGIF EFWHA DGSSTAVK"
gene	471686..472612	/gene="livH"
CDS	471686..472612	/locus-tag="y0423" /gene="livH" /locus-tag="y0423" /function="transport; transport of small molecules; amino acids, amines" /note="residues 1 to 308 of 308 are 87.33 pct identical to residues 1 to 308 of 308 from E. coli K12 : B3457; residues 1 to 308 of 308 are 87.66 pct identical to residues 1 to 308 of 308 from GenPept : >gb AAL22423.1 (AE008864) ABC superfamily (membrane), branched-chain amino acid transporter, high-affinity [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="high-affinity branched-chain amino acid ABC transport system membrane permease" /protein-id="AAM84012.1" /db-xref="GI:21957114" /translation="MSEQFLYFLQQMFNGITLGS TYALIAIGYTMVYGIIGMINFAHG EVYMISSYVSFIVIAALMMVGIDASWLLIGCAFL VSIVIASTYGWSIERVAYKPVRRS"

		KRLIALISAIGMSIFLQNYVSLTQGSRDALAPSL VTGQWTLGESNGFAATISTMQLTI WIVTFLAMLALTLFIRYSRMGRACRACAEDLKMA SLLGINTDRVISLTFVIGALMAAV AGVLLGQFYGVINPYIGFMAGMKAFTAAVLGGIG SIPGAMIGGLVLGVAEALTSAYLS TEYKDAVSFALLIVVLLVMPTGILGRPEVEKV"
gene	472609..473895	/gene="livM" /locus-tag="y0424"
CDS	472609..473895	/gene="livM" /locus-tag="y0424" /function="transport; transport of small molecules; amino acids, amines" /note="residues 1 to 428 of 428 are 79.43 pct identical to residues 1 to 425 of 425 from E. coli K12 : B3456" /codon-start=1 /transl-table=11 /product="inner membrane permease of high-affinity branched-chain amino acid ABC transport system" /protein-id="AAM84013.1" /db-xref="GI:21957115" /translation="MKQLNFVNAIISFVLLVLA SFVMGLQLQLDGTRLVVQGASEVR WLWIGAGCLVVFCFQLVRPLIQQGIKKVSGPAWV LPSFDGTTPRQKLLAAVVIIAAVA WPFLVSRGSVDIATLTLIYVMLGLGLNVVVGLSG LLVLGYGGFYAIGAYTYALLNHYY GLGFWESEPLAGITAALSGFLLGFVLRRLRGDYL AIVTLGFGEIVRILLNNTTEITGG PNGISQIPKPTLFGLEFSRTAKDGGWDTFHNFFG LTYDPSHRIIFLYLVALLLVILT FVINRLLRMPLGRAWEALREDEIACRSLGLSPTK IKLTAFTISAAAFAGFAGTLFAARQ GFVSPESFTFVESAFVLAIVVLGGMGSQFAVILA AVLLVVSRELMRDLNAYSMLLLGA LMVLMMIWRPQGLLPMKRPQLKLKVADVKAKQGE QA"
gene	473892..474659	/gene="livG" /locus-tag="y0425"
CDS	473892..474659	/gene="livG" /locus-tag="y0425" /function="transport; transport of small molecules; amino acids, amines" /note="residues 4 to 255 of 255 are 82.14 pct identical to residues 3 to 254 of 255 from E. coli K12 : B3455; residues 4 to 255 of 255 are 83.33 pct identical to residues 3 to 254 of 255 from GenPept : >gb AAL22421.1 (AE008864) ABC superfamily (atp-bind), branched-chain amino acid transporter, high-affinity [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="ATP-binding component of

		high-affinity branched-chain amino acid ABC transport system"
		/protein-id="AAM84014.1"
		/db-xref="GI:21957116"
		/translation="MNGQPLLTVEGLSMRFGGLL AVNNVGLTLNQGEIVSLIGPNGAG KTTIFNCLTGFYRPTGGTIKLRERHLEGLPGQMI ARMGVIRTFQHVRLEFREMVIENL LVAQHQHLKSGIFAGLLKTPGFRRAEADALARAA TWLERVGLLALANRQAGNLAYGQQ RRLEIARCMVTRPELLMLDEPAAGLNPKETDELN QLIMELRDQHQVSVLLIEHDMKLV MGISDRIYVVNQGTPLAQGLPAEIRNNPDVIRAY LGE"
gene	474674..475405	/gene="livF"
		/locus-tag="y0426"
CDS	474674..475405	/gene="livF"
		/locus-tag="y0426"
		/function="transport; transport of small molecules; amino acids, amines"
		/note="residues 11 to 243 of 243 are 87.12 pct identical to residues 9 to 241 of 241 from E. coli K12 : B3454"
		/codon-start=1
		/transl-table=11
		/product="ATP-binding component of leucine transport"
		/protein-id="AAM84015.1"
		/db-xref="GI:21957117"
		/translation="MESGRGINNNMLSFNQVSAH YGKIQALHQVSLHIQQGEIVTLIG ANGAGKTTLLGTLCEPRATEGNIVFGEQDITHW QTARIMREAIAIVPEGRRVFSRMT VEENLAMGGFFADRQQYQQRIERVYDLFPRLFER RIQRAGTMSGGEQQMLAIGRALMS QPKLLLLDEPSLGLAPIIILQIFDTIQQLREEGM TIFLVEQNANQALKLADRGYVLEN GRIVLEDTGAALLANEAVRSAYLGG"
gene	475633..476094	/locus-tag="y0427"
CDS	475633..476094	/locus-tag="y0427"
		/note="residues 26 to 113 of 153 are 28.40 pct identical to residues 181 to 264 of 413 from GenPept : >gb AAC44570.1 (U61140) ORF1 [Mycoplasma mycoides subsp. mycoides SC]"
		/codon-start=1
		/transl-table=11
		/product="hypothetical"
		/protein-id="AAM84016.1"
		/db-xref="GI:21957118"
		/translation="MMDGISNKMDLQGLSAVRSF AFLTADLMLNITNKNGDNHEYKVT SSHVNNDKLQGPKGILKATKNHAELKNETIASGE KKTISFDKLHVREIPDREQASYID NLSLNRNIYLDTSADRECRIPQVLSPDQNVDSG TKKPFWISKYLCITTLY"
gene	complement (476209..4773 15)	/locus-tag="y0428"
CDS	complement (476209..4773	/locus-tag="y0428"

15)

```
/note="residues 16 to 44 of 368
are 51.61 pct identical to
residues 242 to 272 of 621 from
GenPept : >gb|AAF48396.1|
(AE003497) CG9521 gene product
[Drosophila melanogaster]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM84017.1"
/db-xref="GI:21957119"
/translation="MNIKNKPLLIGLLLLFLHPT
TAAATKWVGNYFYPLANKYSNCNV
TLLEDNSVAVSFDVTLVADLFETDRGPHLQRWKK
IIGTQQDVLVQNNALLFLYFYHA
DGSADFSIRPGDIQNMSLNGIPVQEIDYNLQEAR
FVSTHAFSNQSYHVSFNITANALK
HIRMGATIGGVLHSEGVSYSVRSPQGVAFNQSGN
QCEFFDPTTEIAPSHALYIEPKFR
LGSIAIWQLKSLDLHDHLLDSTADNHGLHAPLVNGP
ANRFCIHYPAGTQNRMYMISASN
LNGLAESSRYFQLKDNQGEHIINYKVTLKNHEDS
EADFSLPKEKKFIQLKSDTSSGGE
AQMCSWSPRIRVYSTDTTDKGHYTDTLNFTITPLA
"
```

```
gene      complement(477393..4779 /locus-tag="y0429"
11)
CDS       complement(477393..4779 /locus-tag="y0429"
11)
```

```
/note="residues 61 to 118 of 172
are 29.31 pct identical to
residues 781 to 838 of 987 from
GenPept : >dbj|BAB75624.1|
(AP003594) ORF-ID:alr3925
hypothetical protein [Nostoc sp.
PCC 7120]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM84018.1"
/db-xref="GI:21957120"
/translation="MNTIKMAITLLLLSWHTCWA
ATPLGDIDVKLEVTAQPRIEIEKP
HGGWYDNIKLHNSPENHAVYEVEVPVAVKLRRQE
GYQISIKNPLILTRQSDAFSAIEQ
TFSPAEVWRGNNRNLRLLSAVPESFSVPPQATR
HTTDDYVLQISAKAPAGDNTAGKY
HGQLTLVFEVNS"
```

```
gene      complement(477973..4786 /locus-tag="y0430"
35)
CDS       complement(477973..4786 /locus-tag="y0430"
35)
```

```
/note="residues 6 to 174 of 220
are 27.27 pct identical to
residues 1 to 173 of 238 from
GenPept : >emb|CAA87760.1|
(Z47800) CotB [Escherichia coli]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM84019.1"
```

		/db-xref="GI:21957121" /translation="MVRWTVKNLVFAAISLLPLS AAGVIDIQPVVELQQVNTVVTVI NHGMTAEYITVQLYRLNNPGVASELESLTPVG YQQPLL FATPLKLT LGPRQSGKIFL HALGAPEQEQVYRLAVVPSNHLKISGNNTAV VGVQISYMGLIRHLPASIQHQWTHRCI AGKPELHNTGNTRLYWHQLQAQQQMIDDFTL YPG RYRQLAFNELQGKVEDQAVNLQCP SG"
gene	complement(478592..479311)	/locus-tag="y0431"
CDS	complement(478592..479311)	/locus-tag="y0431"

```

/note="residues 11 to 221 of 239
are 21.02 pct identical to
residues 3 to 206 of 236 from
GenPept : >emb|CAD08770.1|
(AL627266) putative fimbrial
protein [Salmonella enterica
subsp. enterica serovar Typhi]"
/codon-start=1
/transl-table=11
/product="hypothetical"
/protein-id="AAM84020.1"
/db-xref="GI:21957122"
/translation="MPRRLLPIGTFMKYLYSILS
IALLLAPGSATHGQLLATPTRIAV
EAQELKRTVQVYNSGDTPLYLDITLQRVDNPGVN
PERKTPISEISQPEMIFNPNRITL
GPRQKRDITLIPLKSPVQETLYRLYINPVLNIKA
VGDGEDKSKVHAPMTISIGYGVL I
HHLPPAAAQTRHWQHQCSTTGELTLTATGTVHSK
FKQLESGGNAALADSLNLYPGTAL
TLPVKOLNGEVDGEKESLRCH"

```

```

gene      complement(479296..4816 /locus-tag="y0432"
44)
CDS       complement(479296..4816 /locus-tag="y0432"
44)
          /note="residues 53 to 775 of 782
          are 20.33 pct identical to
          residues 49 to 830 of 869 from
          GenPept : >gb|AAC41416.1| (M55661)
          colonization factor antigen c
          [Escherichia coli]"
          /codon-start=1
          /transl-table=11
          /product="hypothetical"
          /protein-id="AAM84021.1"
          /db-xref="GI:21957123"
          /translation="MEWNPMAYYSKINHSLFFTL
          ALFTLKLAAHAEAVKIEYLVPMGFS
          AAEEENNSLQLLGVLDSKTLPSITFSEEEQQLQF
          NQQNYRHNINISEESIILLGEILSQ
          IPYLQCKTGCDYTLSGHRVALDKVNNTLTITNNN
          NRYLMPPTTTWGLVSNQSLDLRMTA
          AHYRAMSVRGQSYIGLPWQSYGFASWFYNAIQSQ
          NTLQSQNTMPSQSTYQPVNRPQYQ
          RLTQKGIGSWYLQKNFSALYLRTGRQNNLDNNAG
          SVHTLINPALDQFVTLGSQSYLAI
          DKPSTGSIVLYAAQDGDYEIYRDNQLIRRIPAQL
          GRNEIDYSQLPGGYNVEIRLVDR
          LGRIYVOENOTISNIGNOTNNGWFLTMGKGPAGG

```

		KKTPRLVQFGRSRVIESVQTNITL LKDDAHHWAVEANVSRPLSLNKVNITPTGGLMSG EKRSGGYVRLNGGNNTLGYFSLAR YQSPYVSRYAPDSGSTSGSYTRRIGPTQLSYQFN QYRNNRQHRIQSGWDWQLPQFNLA LSLGLQNGGQWN SHNNYGVFLNTTLSFGQSNASI NTAYTQQQLNTSASYQKEFIDNYG ASTLGVSGSASGKLNSVGGFAKRSGSRGDISGRV GIDNQITNGGISYNGMLALSSQGV ALGRSSYSGAALLIKAPALGGTPYSFHVEDSPIT GGGTYAIPVPYQDRFFVTRHTDR SDMDMNIQLPVNIVRAHPGQVFSGEADITLNLly SGFLKNAQGLPVSGVIEETGDTAY PNGLFSINAQNRLQAITVHGPGSGRYRCMDHMQPT HIYLCHAD"
gene	complement (481896..482387)	/locus-tag="y0433"
CDS	complement (481896..482387)	/locus-tag="y0433" /note="residues 3 to 157 of 163 are 26.06 pct identical to residues 4 to 164 of 170 from GenPept : >gb AAC41415.1 (M55661) colonization factor antigen b [Escherichia coli]" /codon-start=1 /transl-table=11 /product="hypothetical" /protein-id="AAM84022.1" /db-xref="GI:21957125" /translation="MMKKTVIAIITMATLTSTAA YANTIEKDIRVEAEIISLMDVKRA DDSNINKIKLTYDTVTNDGTYSHSEAIKVKARKQ LGDKLKVSLAAPVILSEPNNNKEF THVEVLLDGKKLLETADTRDLIAFHGSELNAELK VSAKEPNNNAVGGEEKYSGVIQLRLE PSA"
gene	482942..484261	/gene="ugpB"
		/locus-tag="y0434"
CDS	482942..484261	/gene="ugpB" /locus-tag="y0434" /function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="sn-glycerol 3-phosphate ABC transport system; residues 6 to 439 of 439 are 80.18 pct identical to residues 4 to 437 of 438 from E. coli K12 : B3453; residues 5 to 439 of 439 are 82.06 pct identical to residues 3 to 437 of 438 from GenPept : >gb AAL22417.1 (AE008864) ABC superfamily (peri-perm), sn-glycerol 3-phosphate transport protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="periplasmic binding protein" /protein-id="AAM84023.1" /db-xref="GI:21957126" /translation="MFNNSIHKVSICIALTLTFS

		ANAMAVTEIPFWHSMEGELGKEVD SIADRFNQSQPDYKIVPVYKGNYEQSLAAGIAAF RSGKAPAILQVYEVGTATMMASKA IKPVYQVFKDANIDFDES FVPTVAGYYTDSKTG RLLSQPFNSSTPVLYYNKEAFKKA GLDPEQPPKTWQELAADTAKLRAAGSSCGYASGW QGWIQIENFSAWHGQPIASRNNGF DGTDAVLEFNKPLQVKHIQLLSDMNKKGDFTYFG RKDESTSKFYNGDCAITTASSGSL ASIRHYAKFNFGVGMMPYDADAKNAPQNAIIGGA SLWVMDGKDKEYKGVAEFLQYLV KPEIAAEWHQKTGYLPITTAAYELTKQQGFYEQN PGADVATRQMLNKPPLPYTKGLRL GNMPQIRTVVDEELEAVWTAKKTPQAALDNSVKR GDVLLRRFEQANK"
gene	484559..485446	/gene="ugpA"
		/locus-tag="y0435"
CDS	484559..485446	/gene="ugpA" /locus-tag="y0435" /function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="sn-glycerol 3-phosphate ABC transport system; residues 1 to 295 of 295 are 79.32 pct identical to residues 1 to 295 of 295 from E. coli K12 : B3452; residues 1 to 295 of 295 are 80.33 pct identical to residues 1 to 295 of 295 from GenPept : >gb AAL22416.1 (AE008864) ABC superfamily (membrane), sn-glycerol 3-phosphate transport protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="integral membrane protein, permease" /protein-id="AAM84024.1" /db-xref="GI:21957127" /translation="MSPSRPGFSCSWLPYLLVLP QLAITAIFFLWPAGEALWYSVQTL DPFGLSSEFVGLSNFIQLFQDEYYLASFYTTLIF SALVAGIGLIVSLFLAAMVNYVLR GSRLYQTLILPYAVAPAAVLWIFLFDPLGLL ITHALAKLGYSWNHAQNSGQAMFL VVLASVWKQISYNFLFFLAALQSIPKSLVEAAAI DGAGPVRRFFNLVPLISPVSFFL LVVNLVYAFFDTFPVIDAATGGGPVQATTTLIYK IYREGFAGLDLSSSAAQSVILMLL VIGLTVIQFRFVERKVRVYQ"
gene	485443..486288	/gene="ugpE"
		/locus-tag="y0436"
CDS	485443..486288	/gene="ugpE" /locus-tag="y0436" /function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="sn-glycerol 3-phosphate ABC transport system; residues 1 to 281 of 281 are 77.58 pct identical to residues 1 to 281 of 281 from

		E. coli K12 : B3451; residues 1 to 281 of 281 are 79.71 pct identical to residues 1 to 281 of 281 from GenPept : >gb AAL22415.1 (AE008864) ABC superfamily (membrane),sn-glycerol 3-phosphate transport protein [Salmonella typhimurium LT2]" /codon-start=1 /transl-table=11 /product="inner membrane permease" /protein-id="AAM84025.1" /db-xref="GI:21957128" /translation="MIENRRGLDIFCHIMLIIGV LLILFPLYVAFVAASLDDSQVFQA PMTLIPGPHLWQNISHIWHAGVGNNSTPFGLMLL NSFVMAFAITVGKITVSILSAYAI VYFRFPLRNLFWWLIFLTLMLPVEVRIFPTIEVI ANLNLLDSYTGTLPLMASATATF LFRQFFMTLPDELLEAARIDGAGAMRFFWDIVLP LSKTNLAALFVITFIYGWNQYLWP ILITSDASMGTA VAGIRSMISTSGAPTQWNQVMA AMILT LIPPVVVVLLMQRW FVRGL VDSEK" /gene="ugpC" /locus-tag="y0437"
gene	486295..487368	
CDS	486295..487368	/gene="ugpC" /locus-tag="y0437" /function="transport; transport of small molecules; carbohydrates, organic acids, alcohols" /note="sn-glycerol 3-phosphate ABC transport system; residues 1 to 355 of 357 are 75.56 pct identical to residues 14 to 369 of 369 from E. coli K12 : B3450; residues 1 to 355 of 357 are 75.56 pct identical to residues 14 to 369 of 369 from GenPept : >gb AAG58556.1 AE005568-6 (AE005568) ATP-binding component of sn-glycerol 3-phosphate transport system [Escherichia coli O157:H7 EDL933]" /codon-start=1 /transl-table=11 /product="ATP-binding component" /protein-id="AAM84026.1" /db-xref="GI:21957129" /translation="MACLKLQAVTKSYDGVTPVI KQIDL DVADGEFIVMVGPSGCGKS TLLRMVAGLERTTTGDIYIGDQRVTDLEPKDRGI AMVFQNYVLYPHMNVFDNMAYGLK IRGFGKEQIRQRVDEAARILELQPLLKRKPRELS GGQRQ RVAMGRAIVREPAVFLFDE PLSNLDAKLRVQMLLELQQ LHRR LKTTSLYVTHD QVEAMTLAQRVIVMNKGVAEQIGT PSEVYKRPASLFVASFIGSPAMNLLDGTVSPDGR TFILSDGLTLPLEIPQPQWGGRRL TLGIRPEHIQQTTSAQGVPMNLLTLELLGADNLA HGLWGGQSIIARLSHEEMPVAGST LHLYLPPAALHFFD TDSGLRIEP" /gene="ugpQ"
gene	487365..488114	

```

CDS          487365..488114      /locus-tag="y0438"
                                   /gene="ugpQ"
                                   /locus-tag="y0438"
                                   /function="enzyme; central
                                   intermediary metabolism: Pool,
                                   multipurpose conversions"
                                   /note="residues 4 to 247 of 249
                                   are 72.95 pct identical to
                                   residues 3 to 245 of 247 from E.
                                   coli K12 : B3449; residues 4 to
                                   247 of 249 are 73.77 pct identical
                                   to residues 3 to 245 of 247 from
                                   GenPept :
                                   >gb|AAG58555.1|AE005568-5
                                   (AE005568) glycerophosphodiester
                                   phosphodiesterase, cytosolic
                                   [Escherichia coli O157:H7 EDL933]"
                                   /codon-start=1
                                   /transl-table=11
                                   /product="cytosolic
                                   glycerophosphodiester
                                   phosphodiesterase"
                                   /protein-id="AAM84027.1"
                                   /db-xref="GI:21957130"
                                   /translation="MNRDWPYPPIVAHRGGGSLA
                                   PENTLAAIDVGARYGHKMIEFDAK
                                   LSQDGQIFLLHDDTLERTSNGWGVAGELTWEKLI
                                   QLDAGDWFSKAFRGERLPLLSEVA
                                   ARCAQHGMANIEIKPTTGTDAPTGRAIALAARA
                                   LWQGQPIPLLSSFSVDALAAQQL
                                   AVPELPRGLLLDKWDDNWAALTTQLDCVSLHINH
                                   KQLTAERVALLKAAGLRILVYTVN
                                   QPERARELLNWGVDCICTDRIDLLGSDFGTGC"

```

```

gene          488215
<-----User Break----->

```

```
=> d hist
```

```
(FILE 'HOME' ENTERED AT 04:02:48 ON 01 OCT 2008)
```

```

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, ANTE, AQUALINE,
AQUASCI, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CAPLUS,
CEABA-VTB, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE, DISSABS, DRUGB,
DRUGMONOG2, DRUGU, EMBAL, EMBASE, ...' ENTERED AT 04:03:14 ON 01 OCT 2008
SEA BIOFILM AND REMOV?(P)BIOFILM AND PROTEASE AND ESTERASE AND
-----

```

```

0* FILE ADISNEWS
0* FILE ANTE
0* FILE AQUALINE
0* FILE BIOENG
0* FILE BIOTECHABS
0* FILE BIOTECHDS
0* FILE BIOTECHNO
0* FILE CEABA-VTB
0* FILE CIN
0* FILE ESBIODASE
0* FILE FOMAD
0* FILE FOREGE
0* FILE FROSTI
0* FILE FSTA
1 FILE GENBANK
1 FILE IFIPAT

```

0* FILE KOSMET
0* FILE NTIS
0* FILE NUTRACEUT
0* FILE PASCAL
0* FILE PHARMAML
11 FILE USPATFULL
4 FILE USPAT2
0* FILE WATER

L1 QUE BIOFILM AND REMOV?(P) BIOFILM AND PROTEASE AND ESTERASE AND

FILE 'GENBANK, IFIPAT, USPATFULL, USPAT2' ENTERED AT 04:05:30 ON 01 OCT
2008

L2 17 S L1
L3 13 DUP REM L2 (4 DUPLICATES REMOVED)

=> logoff

ALL L# QUERIES AND ANSWER SETS ARE DELETED AT LOGOFF

LOGOFF? (Y)/N/HOLD:y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	45.35	48.16

STN INTERNATIONAL LOGOFF AT 04:07:12 ON 01 OCT 2008